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We found 64 dictionaries with English definitions that include the word *gene*:

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➤ **General** (19 matching dictionaries)

1. [gene](#) : Merriam-Webster's Online Dictionary, 10th Edition [[home](#), [info](#)]
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3. [gene](#) : Cambridge International Dictionary of English [[home](#), [info](#)]
4. [gene](#) : The Wordsmyth English Dictionary-Thesaurus [[home](#), [info](#)]
5. [gene](#) : The American Heritage® Dictionary of the English Language [[home](#), [info](#)]
6. [gene](#) : Infoplease Dictionary [[home](#), [info](#)]
7. [-gene](#), [gene](#), [gene-](#) : Dictionary.com [[home](#), [info](#)]
8. [Gene](#), [gene](#) : UltraLingua English Dictionary [[home](#), [info](#)]
9. [gene](#) : Cambridge Dictionary of American English [[home](#), [info](#)]
10. [Gene](#) : Wikipedia, the Free Encyclopedia [[home](#), [info](#)]
11. [gene](#) : Rhymezone [[home](#), [info](#)]
12. [gene](#), [gene](#) : AllWords.com Multi-Lingual Dictionary [[home](#), [info](#)]
13. [gene](#) : All About Homonyms [[home](#), [info](#)]
14. [gene](#) : Columbia Encyclopedia, Six Edition [[home](#), [info](#)]
15. [gene](#) : The New Dictionary of Cultural Literacy [[home](#), [info](#)]
16. [Gene](#) : Encarta® Online Encyclopedia, North American Edition [[home](#), [info](#)]
17. [gene](#) : WordNet 1.7 Vocabulary Helper [[home](#), [info](#)]
18. [gene](#) : LookWAYup Translating Dictionary/Thesaurus [[home](#), [info](#)]
19. [gene](#) : Encyclopedia.com [[home](#), [info](#)]

➤ **Art** (1 matching dictionary)

Quick definitions (*Gene*)

- **noun:** (genetics) a segment of DNA that is involved in producing a polypeptide chain; it can include regions preceding and following the coding DNA as well as introns between the exons; it is considered a unit of heredity (Example: "Genes were formerly called factors")
- **name:** A male given name (common: 1 in 1149 males; popularity rank in the U.S.: #200)
- **name:** A female given name (rare: 1 in 20000 females; popularity rank in the U.S.: #1299)
- **name:** A surname (very rare: popularity rank in the U.S.: #40659)

Encyclopedia article

The word "**gene**" is shared by many

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 26.6667 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ1

Perfect score: 56
Sequence: 1 gytftsydin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	83.9	448	16 Q8A516	Q8A516 bacteroides
2	47	83.9	480	11 Q8K024	Q8K024 mus musculus
3	47	83.9	497	4 Q8WY24	Q8WY24 homo sapien
4	45	80.4	147	11 Q925S3	Q925S3 mus musculus
5	43	76.8	473	11 Q9D8L4	Q9D8L4 mus musculus
6	42	75.0	241	11 Q921A6	Q921A6 mus musculus
7	42	75.0	481	11 Q91WY1	Q91WY1 mus musculus
8	41	73.2	550	5 Q02490	Q02490 tritrichomo
9	40	71.4	102	5 Q9VF36	Q9VF36 drosophila
10	40	71.4	109	11 Q9JL75	Q9JL75 mus musculus
11	40	71.4	119	5 Q9GY22	Q9GY22 schistosoma
12	40	71.4	120	11 Q920E8	Q920E8 mus musculus
13	40	71.4	123	11 Q8VJ11	Q8VJ11 mus musculus
14	40	71.4	137	11 Q924R6	Q924R6 mus musculus
15	40	71.4	139	11 Q924R5	Q924R5 mus musculus
16	40	71.4	140	11 Q924P8	Q924P8 mus musculus

17	40	71.4	140	11 Q924R2	Q924R2 mus musculus
18	40	71.4	141	11 Q924Q4	Q924Q4 mus musculus
19	40	71.4	142	11 Q924Q1	Q924Q1 mus musculus
20	40	71.4	142	11 Q924Q2	Q924Q2 mus musculus
21	40	71.4	143	11 Q91VA2	Q91VA2 mus musculus
22	40	71.4	143	11 Q924Q5	Q924Q5 mus musculus
23	40	71.4	143	11 Q91V67	Q91V67 mus musculus
24	40	71.4	143	11 Q924Q0	Q924Q0 mus musculus
25	40	71.4	143	11 Q924R7	Q924R7 mus musculus
26	40	71.4	143	11 Q924P6	Q924P6 mus musculus
27	40	71.4	143	11 Q924R0	Q924R0 mus musculus
28	40	71.4	143	11 Q924P9	Q924P9 mus musculus
29	40	71.4	144	11 Q924P5	Q924P5 mus musculus
30	40	71.4	145	11 Q924Q6	Q924Q6 mus musculus
31	40	71.4	145	11 Q924Q9	Q924Q9 mus musculus
32	40	71.4	145	11 Q924R3	Q924R3 mus musculus
33	40	71.4	145	11 Q924Q7	Q924Q7 mus musculus
34	40	71.4	145	11 Q924P7	Q924P7 mus musculus
35	40	71.4	145	11 Q924R1	Q924R1 mus musculus
36	40	71.4	145	11 Q924R4	Q924R4 mus musculus
37	40	71.4	146	11 Q924R8	Q924R8 mus musculus
38	40	71.4	146	11 Q924Q3	Q924Q3 mus musculus
39	40	71.4	146	11 Q924Q8	Q924Q8 mus musculus
40	40	71.4	278	11 Q921K1	Q921K1 mus musculus
41	40	71.4	482	11 Q8K172	Q8K172 mus musculus
42	40	71.4	486	11 Q91207	Q91207 mus musculus
43	40	71.4	488	11 Q8K0F2	Q8K0F2 mus musculus
44	40	71.4	1061	5 Q9GUL6	Q9GUL6 caenorhabdi
45	39	69.6	118	4 Q9UL91	Q9UL91 homo sapien

ALIGNMENTS

RESULT 1

Q8A516 PRELIMINARY; PRT; 448 AA.
AC Q8A516;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative outer membrane protein TolC.
GN BT253.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550558; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RT Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; A016935; AA077360.1; -;
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0005810; P:transport; IEA.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OEP; 2.
KW Complete proteome.
SQ SEQUENCE 448 AA; 51254 MW; E4DA4539991DFB28 CRC64;

Query Match 83.9%; Score 47; DB 16; Length 448;
Best Local Similarity 80.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYTFTSYDIN 10
Db 299 GYTFNKYDIN 308

RESULT 2

Q8K0Z4 Q8K0Z4 PRELIMINARY; PRT; 480 AA.
 AC Q8K0Z4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to expressed sequence AI833585.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Breast tumor;
 RA Strausberg R.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029188; AAH29188.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 83.9%; Score 47; DB 11; Length 480;
 Best Local Similarity 80.0%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTSYDIN 10
 |||||:
 Db 45 GYFTSYDIN 54

RESULT 3
 Q8WY24 Q8WY24 PRELIMINARY; PRT; 497 AA.
 AC Q8WY24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SMC66 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
 RT Identification and characterization of SMC66, a Ig-like gene which is
 RT down-regulated in colorectal cancer."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF283666; AAL36987.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 83.9%; Score 47; DB 4; Length 497;
 Best Local Similarity 80.0%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTSYDIN 10
 |||||:
 Db 45 GYFTSYDIN 54

Db 45 GYFTSYDIN 54
 RESULT 4
 Q925S3 Q925S3 PRELIMINARY; PRT; 147 AA.
 AC Q925S3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MRP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RT Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after irradiation in mice."
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain."
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240166; AAK43731.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 80.4%; Score 45; DB 11; Length 147;
 Best Local Similarity 80.0%; Pred. No. 2.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYFTSYDIN 10
 |||||:
 Db 28 GYFTSYDIN 37

RESULT 5
 Q9D8L4 Q9D8L4 PRELIMINARY; PRT; 473 AA.
 AC Q9D8L4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 181006009Rik protein.
 GN IGH-1 OR 181006009RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Akaiwa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Akaiwa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wegner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK007918; BAE25349.1; -.
 DR PIR: S26746; S26746.
 DR HSSP: P01842; 7FAB.
 DR MGD: MGI:96443; Igh-1.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 76.8%; Score 43; DB 11; Length 473;
 Best Local Similarity 80.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYTFSTYDIN 10
 Db 45 GYTFDYDYN 54

RESULT 6
 Q921A6 PRELIMINARY; PRT; 241 AA.
 AC Q921A6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-CEA 79 single chain Fv fragment (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98170165; PubMed=9509426;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
 RT "Cloning and characterization of cDNAs encoding VH and VL of a
 RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
 RT generation of a single-chain Fv molecule (scFv).";
 RL Mol. Cells 7:816-819(1997).
 DR EMBL: U88067; AAB48044.1; -.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00406; IGV; 2.
 DR PROSITE: PS00835; IG_LIKE; 2.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 75.0%; Score 42; DB 11; Length 241;
 Best Local Similarity 70.0%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYTFSTYDIN 10
 Db 26 GYTFDYDYN 35

RESULT 7
 Q91WT1 PRELIMINARY; PRT; 481 AA.
 ID Q91WT1
 AC Q91WT1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL EMBL: BC013490; AAH13490.1; -.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Hypothetical protein
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 75.0%; Score 42; DB 11; Length 481;
 Best Local Similarity 80.0%; Pred. No. 29;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFSTYDIN 10
 Db 45 GYTFSTYDIN 54

RESULT 8
 O02490 PRELIMINARY; PRT; 550 AA.
 ID O02490
 AC O02490;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fructofuranosidase (EC 3.2.1.26).
 OS Trichomonas foetus (Trichomonas foetus).
 OC Eukaryota; Parabasalida; Trichomonadida; Trichomonadidae;
 OC Trichomonadinae; Trichomonas.
 OX NCBI_TaxID=5724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT85-330.1;
 RA Granger B.L., Hillemeier P.B., Warwood S.J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 DR EMBL: U66071; AAB51115.1; -.
 DR EMBL: U66071; AAB51117.1; -.
 DR GO: GO:0004564; F:beta-fructofuranosidase activity; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR001362; Glyco_hydro_32.
 DR Pfam: PF00251; Glyco_hydro_32; 1.
 DR SMART: SM00640; Glyco_32; 1.
 DR PROSITE: PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW Glycoprotein; Glycosidase; Hydrolase.
 SQ SEQUENCE 550 AA; 62598 MW; 4BA2DF706E1B4438 CRC64;

Query Match 73.2%; Score 41; DB 5; Length 550;
 Best Local Similarity 70.0%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYTFSTYDIN 10

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Db      222 GYTFKYNN 231
||||| | |
RESULT 9
Q9VVF36 PRELIMINARY; PRT; 102 AA.
AC Q9VVF36;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cg18505 protein.
GN ACY22 OR Cg18505.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Fiankoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista A.B., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003710; AAF55224.1; -
DR HSSP; P41500; 2ACY.
DR FlyBase; FBgn0038363; ACY22.
DR GO; GO:0003998; Fcylphosphatase activity; IEA.
DR InterPro; IPR001792; Acylphosphatase.
DR Pfam; PF00708; Acylphosphatase; 1.
DR PRINTS; PR00112; ACYLPHPTASE.
DR ProDom; PD001884; ACYLPHPTASE; 1.
DR PROSITE; PS00150; ACYLPHOSPHATASE 1; 1.
DR SEQUENCE 102 AA; 11765 MW; 3CD509E7FF96FEDE CRC64;

Query Match 71.4%; Score 40; DB 5; Length 102;
Best Local Similarity 87.5%; Pred. No. 13;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YTFYSYDI 9
      ||||| | |
Db      93 YTFISFDI 100

RESULT 10
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206031; AAF69329.1; -
DR PIR; S26312; S26312.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 71.4%; Score 40; DB 11; Length 109;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYTFYSY 7
      ||||| | |
Db      17 GYTFISY 23

RESULT 11
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -
DR HSSP; P01772; 2FBJ.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 71.4%; Score 40; DB 5; Length 119;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFTTSYDIN 10
Db 26 GYSFTGYNN 35

RESULT 12
Q920E8 PRELIMINARY; PRT; 120 AA.
AC Q920E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL EMBL; AF307936; AAL09420.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 71.4%; Score 40; DB 11; Length 120;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTTSYDIN 10
Db 26 GYSFTGYNN 35

RESULT 13
Q8VIJ1 PRELIMINARY; PRT; 123 AA.
AC Q8VIJ1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-DNA heavy chain (Fragment).
GN J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96409289; PubMed=6814271;
RX STRAIN=C3H/HeJ-lpr/lpr;

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RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59154; AAB02916.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;

Query Match 71.4%; Score 40; DB 11; Length 123;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTTSYDIN 10
Db 26 GYSFTGYNN 35

RESULT 14
Q924R6 PRELIMINARY; PRT; 137 AA.
AC Q924R6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RC Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067783; BAB63268.1; -.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 137

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SQ SEQUENCE 137 AA; 15171 MW; 5C38D96DC6A4124 CRC64;
 Query Match 71.4%; Score 40; DB 11; Length 137;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTTSY 7
 Db 26 GYTTSY 32

RESULT 15
 Q924RS PRELIMINARY; PRT; 139 AA.
 AC Q924RS;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067784; BAB63269.1; -
 DR PIR; PH1137; PH1137;
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 139 139
 SQ SEQUENCE 139 AA; 15221 MW; 8491E2F85614736A CRC64;

Query Match 71.4%; Score 40; DB 11; Length 139;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTTSY 7
 Db 26 GYTTSY 32

Search completed: April 21, 2004, 17:37:13
 Job time : 28.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 5.07246 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: SEQ1
Perfect score: 56
Sequence: 1 gytftsytidin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	117	1 HV52_MOUSE	P06327 mus musculu
2	49	87.5	120	1 HV03_MOUSE	P01747 mus musculu
3	49	87.5	140	1 HV02_MOUSE	P01746 mus musculu
4	41	73.2	533	1 INV_DEBOC	P24133 debaryomyce
5	40	71.4	114	1 HV00_MOUSE	P01741 mus musculu
6	40	71.4	117	1 HV04_MOUSE	P01748 mus musculu
7	40	71.4	117	1 HV05_MOUSE	P01749 mus musculu
8	40	71.4	117	1 HV06_MOUSE	P01750 mus musculu
9	40	71.4	117	1 HV09_MOUSE	P01753 mus musculu
10	40	71.4	117	1 HV10_MOUSE	P01754 mus musculu
11	40	71.4	117	1 HV49_MOUSE	P06328 mus musculu
12	40	71.4	118	1 HV51_MOUSE	P06330 mus musculu
13	40	71.4	120	1 HV50_MOUSE	P06329 mus musculu
14	40	71.4	137	1 HV11_MOUSE	P01755 mus musculu
15	40	71.4	139	1 HV07_MOUSE	P01751 mus musculu
16	40	71.4	946	1 IHB_DROME	O61643 drosophila
17	39	69.6	117	1 HV14_MOUSE	P01758 mus musculu
18	39	69.6	532	1 INV1_YEAST	P10594 saccharomyc
19	39	69.6	532	1 INV2_YEAST	P00724 saccharomyc
20	39	69.6	532	1 INV4_YEAST	P10596 saccharomyc
21	38	67.9	217	1 COAT_PSVJ	P22116 peanut stun
22	38	67.9	229	1 COAT_TAV	P23627 tomato aspe
23	38	67.9	409	1 EF1G_SCHPO	P40921 schizosacch
24	37	66.1	121	1 HV01_MOUSE	P01745 mus musculu
25	37	66.1	1383	1 NPC1_CABEL	O19127 caenorhabdi
26	37	66.1	1398	1 PLS_PYRPU	P72186 pyrococcus
27	36	64.3	117	1 HV12_MOUSE	P01756 mus musculu
28	36	64.3	117	1 HV13_MOUSE	P01757 mus musculu
29	36	64.3	117	1 HV16_HUMAN	P23083 homo sapien
30	36	64.3	136	1 HV15_MOUSE	P01759 mus musculu
31	36	64.3	531	1 PYRG_SULTO	Q97669 sulfobolus
32	36	64.3	1256	1 MRP_STRSU	P32653 streptococc
33	35	62.5	117	1 HV15_HUMAN	P01743 homo sapien

34	35	62.5	117	1 HV55_MOUSE	P18526 mus musculu
35	35	62.5	218	1 COAT_CMVAS	O66154 cucumber mo
36	35	62.5	242	1 YHIW_ECOLI	P37638 escherichia
37	35	62.5	465	1 EGLC_RHIME	Q823q2 rhizobium m
38	35	62.5	525	1 YMJ6_YEAST	Q04489 saccharomyc
39	35	62.5	534	1 FM2_ACTNA	P12616 actinomyc
40	35	62.5	550	1 INV1_HAVAN	P40912 hansecula a
41	35	62.5	591	1 LAC1_CRYPA	Q03966 cryphonectr
42	35	62.5	663	1 MNE1_YEAST	P24720 saccharomyc
43	35	62.5	988	1 BLM_CABEL	O18017 caenorhabdi
44	34	60.7	120	1 HV3E_HUMAN	P01766 homo sapien
45	34	60.7	169	1 MOAB_BACAA	Q81k13 bacillus an

ALIGNMENTS

RESULT 1					
HV52_MOUSE					
ID	HV52_MOUSE	STANDARD;	PRT;	117 AA.	
AC	P06327;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V region VH558 Al/A4 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]_TaxID=10090;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85099340; PubMed=2578321;				
RA	Yancopoulos G.D., Alt F.W.;				
RT	"Developmentally controlled and tissue-specific expression of				
RT	unrearranged VH gene segments.";				
RL	Cell 40:271-281(1985).				
CC	-----				
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CC	-----				
DR	EMBL; M13787; AAA38499.1; -				
DR	PIR; A02029; HVMSA1.				
DR	HSSP; P01810; 2FBU.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig_1.				
DR	SMART; SM00406; Igv; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	19		
FT	CHAIN	20	117		
FT	DOMAIN	20	49		
FT	DOMAIN	50	54		
FT	DOMAIN	55	68		
FT	DOMAIN	69	85		
FT	DOMAIN	86	117		
FT	DISULFID	41	115		
FT	NON_TER	117	117		
SQ	SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;				

Query Match 100.0%; Score 56; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.0013; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GYTFTSYDIN 10

|||||

45 GYTFTSYDIN 54

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RESULT 2
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8311846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 87.5%; Score 49; DB 1; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 25 GYTFSTSYGIN 34

RESULT 3
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RA Sime J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; X17604; CAA35606.1; --
CC PIR; S13528; S13528.
CC InterPro; IPR001362; Glyco_hydro_32.
CC Pfam; PF00251; Glyco_hydro_32; 1.
CC SMART; SM00640; Glyco_32; 1.
CC PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 533 INVERTASE.
FT ACT_SITE 50 50 BY SIMILARITY.

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CC EMBL; J00493; AAA38128.1; --
CC PIR; A94284; HVMSG7.
CC HSP; P01810; 2FBU.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 87.5%; Score 49; DB 1; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 45 GYTFSTSYGIN 54

RESULT 4
ID INV DEBOC STANDARD; PRT; 533 AA.
AC P24133;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Invertase precursor (EC 3.2.1.26) (Beta-fructofuranosidase)
DE (Saccharase).
DE INV.
OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=27300;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 2076;
RX MEDLINE=90090692; PubMed=2688929;
RA Klein R.D., Poorman R.A., Favreau M.A., Shea M.H.,
RA Hatzenbuehler N.T., Nulf S.C.;
RT "Cloning and sequence analysis of the gene encoding invertase from
RT the yeast Schwanniomyces occidentalis.";
RL Curr. Genet. 16:145-152(1989).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
CC fructofuranoside residues in beta-D-fructofuranosides.
CC -!- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
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CC or send an email to license@isb-sib.ch).
CC EMBL; X17604; CAA35606.1; --
CC PIR; S13528; S13528.
CC InterPro; IPR001362; Glyco_hydro_32.
CC Pfam; PF00251; Glyco_hydro_32; 1.
CC SMART; SM00640; Glyco_32; 1.
CC PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 533 INVERTASE.
FT ACT_SITE 50 50 BY SIMILARITY.

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FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 533 AA; 60839 MW; C7CB833F30778088 CRC64;

Query Match
Best Local Similarity 73.2%; Score 41; DB 1; Length 533;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYTFSTYDIN 10
DB 158 GYTFSTYDIN 167

RESULT 5
HV00 MOUSE
ID HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D.; Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype."
RL J. Immunol. 123:279-284 (1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02022; GIMSAA.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 106
FT NON TER 114 114 IG-LIKE.
SQ SEQUENCE 114 AA; 12555 MW; 99DDF0B6A69F48E CRC64;

Query Match
Best Local Similarity 71.4%; Score 40; DB 1; Length 114;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTYDI 9
DB 26 GYTFSSYEL 34

RESULT 6
HV04 MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637 (1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match
Best Local Similarity 71.4%; Score 40; DB 1; Length 117;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTY 7
DB 45 GYTFSTY 51

RESULT 7
HV05 MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637 (1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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 DR EMBL; J00536; AAA38605.1; --
 DR FIR; A02031; HVMS3.
 DR HSP; P01810; 2FBJ.
 DR MGD; MGI:96486; Igh-VJ558.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 13016 MW; 427C861CS3975EDC CRC64;

Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 1 GYFTTSY 7
 DB 45 GYFTTSY 51

RESULT 8
 HV06 MOUSE
 ID HV06 MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies; somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR; A02032; HVMS02.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.

FT NON TER 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
 Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 1 GYFTTSY 7
 DB 45 GYFTTSY 51

RESULT 9
 HV09 MOUSE
 ID HV09 MOUSE STANDARD; PRT; 117 AA.
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 186-1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies; somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR; D90809; HVMS61.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 1 GYFTTSY 7
 DB 45 GYFTTSY 51

RESULT 10
 HV10 MOUSE
 ID HV10 MOUSE STANDARD; PRT; 117 AA.
 AC P01754; P11270;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig heavy chain V region 145 precursor.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus.
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6789376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RA "Heavy chain variable region contribution to the NPb family of
 RT antibodies; somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981)
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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 CC -----
 CC EMBL; J00533; AAA38602.1; --
 DR PIR; C90809; HVMS45.
 DR HSSP; P01810; 2FBJ.
 DR MGD; MGI:196486; Igh-VJ558.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT NON_TER 117 117
 FT DISULFID 41 115
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12921 MW; D37D58A3F543E996 CRC64;
 Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYTFSTY 7
 DB 45 GYTFSTY 51
 RESULT 11
 HV49_MOUSE
 ID HV49_MOUSE STANDARD; PRT; 117 AA.
 AC P06328;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region VH558 B4 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8509340; PubMed=2578321;
 RT Yancopoulos G.D., Alt F.W.;
 RA "Developmentally controlled and tissue-specific expression of
 RT unrearranged VH gene segments.";
 RL Cell 40:271-281(1985).
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 CC -----
 CC EMBL; M13788; AAA38506.1; --
 DR PIR; A02035; MHMSB4.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT NON_TER 117 117
 FT DISULFID 41 115
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;
 Query Match 71.4%; Score 40; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYTFSTY 7
 DB 45 GYTFSTY 51
 RESULT 12
 HV51_MOUSE
 ID HV51_MOUSE STANDARD; PRT; 118 AA.
 AC P06330;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region AC38 205.12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=84182519; PubMed=6201362;
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes.";
 RL EMBO J. 3:517-523(1984).
 DR PIR; A02040; MHMS38.
 DR HSSP; P01789; LMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 98
 FT CHAIN 99 104 V SEGMENT.
 FT DOMAIN 105 118 D SEGMENT.
 FT DISULFID 122 96 J SEGMENT.
 FT NON_TER 118 118 BY SIMILARITY.
 SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
 Query Match 71.4%; Score 40; DB 1; Length 118;
 Best Local Similarity 70.0%; Pred. No. 1.3;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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CC -----
CC EMBL; J00539; AAA38172.1; -
CC PIR; A02038; G2MS43.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG-LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 13
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC FRAMEWORK-1.
CC COMPLEMENTARITY-DETERMINING-1.
CC FRAMEWORK-2.
CC COMPLEMENTARITY-DETERMINING-2.
CC FRAMEWORK-3.
CC D SEGMENT.
CC JH2 SEGMENT.
CC BY SIMILARITY.
CC FT DOMAIN 123 137
CC FT DISULFID 41 115
CC FT NON TER 137 137
CC SQ SEQUENCE 137 AA; 15200 MW; ADDS861BF44B9EC9 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTSY 7
Db 45 GYFTSY 51

RESULT 15
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BI-8/186-2 precursor.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1991).
CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00529; AAA38170.1; -

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DR PIR; A90809; MEMS18.
 DR PDB; 1A6U; 27-MAY-98.
 DR PDB; 1A6W; 15-JUL-98.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DOMAIN 118 124
 FT DOMAIN 125 139
 FT DISULFID 41 115
 FT NON TER 139 139
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
 IG HEAVY CHAIN V REGION B1-8/186-2.
 FRAMEWORK-1.
 COMPLEMENTARITY-DETERMINING-1.
 FRAMEWORK-2.
 COMPLEMENTARITY-DETERMINING-2.
 FRAMEWORK-3.
 D SEGMENT.
 JH2 SEGMENT.
 BY SIMILARITY.

Query Match 71.4%; Score 40; DB 1; Length 139;
 Best Local Similarity 100.0%; Pred. NO. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTY 7
 Db 45 GYTFSTY 51

Search completed: April 21, 2004, 17:33:56
 Job time : 6.07246 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 9.13043 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ1
Perfect score: 56

Sequence: 1 gyfttsydin 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	98	2 S26918	Ig heavy chain V r
2	56	100.0	110	2 PH1670	Ig heavy chain V r
3	56	100.0	117	1 HVMSA1	Ig heavy chain pre
4	56	100.0	127	2 S34014	Ig heavy chain V r
5	56	100.0	136	2 S31600	Ig heavy chain V r
6	53	94.6	111	2 PH0988	Ig heavy chain V r
7	51	91.1	132	2 S31556	Ig heavy chain V r
8	49	87.5	76	2 B28572	Ig heavy chain V r
9	49	87.5	98	2 B24754	Ig heavy chain V r
10	49	87.5	98	2 A28572	Ig heavy chain V r
11	49	87.5	102	2 PH1490	Ig heavy chain V r
12	49	87.5	102	2 PH1491	Ig heavy chain V r
13	49	87.5	102	2 S42176	Ig gamma chain V r
14	49	87.5	114	2 PH1522	Ig heavy chain V r
15	49	87.5	114	2 PH1523	Ig heavy chain V r
16	49	87.5	118	2 S38565	Ig heavy chain V r
17	49	87.5	118	2 A24754	Ig heavy chain V r
18	49	87.5	119	2 PH1517	Ig heavy chain V r
19	49	87.5	119	2 PH1518	Ig heavy chain V r
20	49	87.5	119	2 PH1504	Ig heavy chain V r
21	49	87.5	119	2 PH1500	Ig heavy chain V r
22	49	87.5	119	2 PH1502	Ig heavy chain V r
23	49	87.5	119	2 PH1503	Ig heavy chain V r
24	49	87.5	119	2 PH1505	Ig heavy chain V r
25	49	87.5	119	2 PH1520	Ig heavy chain V r
26	49	87.5	119	2 PH1510	Ig heavy chain V r
27	49	87.5	121	2 A26405	Ig heavy chain V r
28	49	87.5	121	2 A21854	Ig heavy chain V r
29	49	87.5	135	2 PH1494	Ig heavy chain V r

RESULT 1

S26918 Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26918

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z12317; NID:G32857; PIDN:CAA78187.1; PID:G32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 56; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10

DB 26 GYTFTSYDIN 35

RESULT 2

PH1670 Ig heavy chain V region (clone 2A12) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1670

R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl

A:Reference number: PH1642; MUID:9301610; PMID:8315388

A:Accession: PH1670

A:Molecule type: mRNA

A:Residues: 1-110 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 56; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10

DB 26 GYTFTSYDIN 35

```

Db      18 GYFTSYDIN 27

RESULT 3
HVM5A1
IG heavy chain precursor V region (A1/A4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999
C/Accession: A02029
R/Yancopoulos, G.D.; Alt, F.W.
Cell 40, 271-281, 1985
A/Title: Developmentally controlled and tissue-specific expression of unrearranged V-H g
A/Reference number: A90860; MUID:85099340; PMID:2578321
A/Accession: A02029
A/Molecule type: DNA
A/Residues: 1-117 <V>
A/Cross-references: GB:M13787; NID:G196006; PIDN:AAA38499.1; PID:G466291
A/Note: the sequence was determined from the germline gene
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <MAT>
F:20-49/Region: framework 1
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:55-68/Region: framework 2
F:69-85/Region: complementarity-determining 2
F:86-117/Region: framework 3
F:41-115/Disulfide bonds: #status predicted

Query Match      100.0%; Score 56; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTSYDIN 10
      |||||
Db      45 GYFTSYDIN 54

RESULT 4
S34014
IG heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S34014; S30535
R/Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A/Reference number: S34001; MUID:93209281; PMID:7681398
A/Accession: S34014
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127 <VAR>
A/Cross-references: EMBL:Z18321
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 56; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTSYDIN 10
      |||||
Db      26 GYFTSYDIN 35

RESULT 5
S31600
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31600

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R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31600
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-136 <CUI>
A/Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 56; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTSYDIN 10
      |||||
Db      45 GYFTSYDIN 54

RESULT 6
PH0988
IG heavy chain V region (clone 178-c3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH0988
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH0988
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-111 <TIL>
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      94.6%; Score 53; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.022;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTSYDIN 10
      |||||
Db      26 GYFTSYDIN 35

RESULT 7
S31596
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31596
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31596
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-132 <CUI>
A/Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      91.1%; Score 51; DB 2; Length 132;
Best Local Similarity 90.0%; Pred. No. 0.06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GYTFTSYDIN 10
 |||||
 Db 45 GYTFTSYDID 54

RESULT 8

B28572
 IG heavy chain V regions (CR-Id 7, CR-Id 14) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jul-2000
 C:Accession: B28572
 R:Siekevitz, M.; Huang, S.Y.; Geffer, M.L.
 Eur. J. Immunol. 13, 123-132, 1983
 A>Title: The genetic basis of antibody production: a single heavy chain variable region
 A:Reference number: A91262; MUID:83157801; PMID:6403356
 A:Accession: B28572
 A:Molecule type: DNA
 A:Residues: 1-76 <SIE>
 A:Cross-references: GB:K02154; GB:M17032; NID:9196176; PIDN:AAA38613.1; PID:g196177
 A>Note: this sequence was determined from the germline gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 76;
 Best Local Similarity 90.0%; Pred. No. 0.078; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 11 GYTFTSYGIN 20

RESULT 9

B24754
 IG heavy chain V region (SE1.3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Sep-1987 #sequence_revision 06-Nov-1992 #text_change 16-Aug-1996
 C:Accession: B24754
 R:Haba, S.; Rosen, E.M.; Meek, K.; Nisonoff, A.
 J. Exp. Med. 164, 291-302, 1986
 A:Reference number: A24754; MUID:86253060; PMID:3088196
 A:Accession: B24754
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-98 <HAB>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 98;
 Best Local Similarity 90.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 9 GYTFTSYGIN 18

RESULT 10

A28572
 IG heavy chain V region (II CR-Id 11) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
 C:Accession: A28572
 R:Siekevitz, M.; Huang, S.Y.; Geffer, M.L.
 Eur. J. Immunol. 13, 123-132, 1983
 A>Title: The genetic basis of antibody production: a single heavy chain variable region
 A:Reference number: A91262; MUID:83157801; PMID:6403356
 A:Accession: A28572
 A:Molecule type: DNA
 A:Residues: 1-98 <SIE>
 A>Note: this sequence was determined from the germline gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 98;
 Best Local Similarity 90.0%; Pred. No. 0.1; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYGIN 35

RESULT 11

PH1490
 IG heavy chain V region (clone XR6-1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1490
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
 A:Reference number: PH1482; MUID:93171820; PMID:8436910
 A:Accession: PH1490
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-102 <GIU>
 A:Experimental source: hybridoma cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 102;
 Best Local Similarity 90.0%; Pred. No. 0.11; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 7 GYTFTSYGIN 16

RESULT 12

PH1491
 IG heavy chain V region (clone XR26-3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1491
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
 A:Reference number: PH1482; MUID:93171820; PMID:8436910
 A:Accession: PH1491
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-102 <GIU>
 A:Experimental source: hybridoma cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 102;
 Best Local Similarity 90.0%; Pred. No. 0.11; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 7 GYTFTSYGIN 16

RESULT 13

S42176
 IG gamma chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
 C:Accession: S42176

R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7651608
A;Accession: S42176
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <MOJ>
A;Cross-references: EMBL:225441; NID:9407810; PID:9407811
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-96/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 102;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 26 GYTFDYDMN 35

RESULT 14
PHI522
IG heavy chain V region (clone PH14-3-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PHI522
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PHI482; MUID:93171820; PMID:8436910
A;Accession: PHI522
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-114 <GIU>
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 114;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 29 GYTFTSYGIN 38

RESULT 15
PHI523
IG heavy chain V region (clone PH18-1-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PHI523
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PHI482; MUID:93171820; PMID:8436910
A;Accession: PHI523
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-114 <GIU>
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 114;
Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 29 GYTFTSYGIN 38

Search completed: April 21, 2004, 17:38:27
Job time : 10.1304 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:33:24 ; Search time 148.696 Seconds
(without alignments)
65.641 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gyftsydin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending_Patents_AA_Main:*
- 1: /cgn2_6/prodata/2/paa/PCTUS COMB.pep:*
 - 2: /cgn2_6/prodata/2/paa/US06 COMB.pep:*
 - 3: /cgn2_6/prodata/2/paa/US07 COMB.pep:*
 - 4: /cgn2_6/prodata/2/paa/US08 COMB.pep:*
 - 5: /cgn2_6/prodata/2/paa/US081 COMB.pep:*
 - 6: /cgn2_6/prodata/2/paa/US082 COMB.pep:*
 - 7: /cgn2_6/prodata/2/paa/US083 COMB.pep:*
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 - 22: /cgn2_6/prodata/2/paa/US097B COMB.pep:*
 - 23: /cgn2_6/prodata/2/paa/US098 COMB.pep:*
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 - 25: /cgn2_6/prodata/2/paa/US099B COMB.pep:*
 - 26: /cgn2_6/prodata/2/paa/US100 COMB.pep:*
 - 27: /cgn2_6/prodata/2/paa/US101 COMB.pep:*
 - 28: /cgn2_6/prodata/2/paa/US102 COMB.pep:*
 - 29: /cgn2_6/prodata/2/paa/US103 COMB.pep:*
 - 30: /cgn2_6/prodata/2/paa/US104 COMB.pep:*
 - 31: /cgn2_6/prodata/2/paa/US106 COMB.pep:*
 - 32: /cgn2_6/prodata/2/paa/US107 COMB.pep:*
 - 33: /cgn2_6/prodata/2/paa/US60 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

RESULT 1
PCT-US03-38234-125
; Sequence 125, Application PC/TUS0338234
; GENERAL INFORMATION:
; APPLICANT: Abgenix, Inc.
; APPLICANT: Lexicon Genetics Incorporated
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: PCT/US03/38234
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125

1	56	100.0	10	1	PCT-US03-38234-125	Sequence 125, App
2	56	100.0	10	32	US-10-726-332-125	Sequence 125, App
3	56	100.0	92	1	PCT-US01-00663-34182	Sequence 34182, A
4	56	100.0	92	23	US-09-864-761-47202	Sequence 47202, A
5	56	100.0	92	27	US-10-182-997-24903	Sequence 24903, A
6	56	100.0	92	28	US-10-203-135-33269	Sequence 33269, A
7	56	100.0	92	28	US-10-203-136-34115	Sequence 34115, A
8	56	100.0	92	28	US-10-203-137-34182	Sequence 34182, A
9	56	100.0	96	1	PCT-US03-22011-3	Sequence 3, Appli
10	56	100.0	96	27	US-10-194-975-3	Sequence 43, Appli
11	56	100.0	98	1	PCT-US03-38450-43	Sequence 289, App
12	56	100.0	98	1	PCT-US03-00398-289	Sequence 290, App
13	56	100.0	98	1	PCT-US03-00398-290	Sequence 285, App
14	56	100.0	98	1	PCT-US03-00398-295	Sequence 296, App
15	56	100.0	98	1	PCT-US03-00398-296	Sequence 342, App
16	56	100.0	98	1	PCT-US03-00398-342	Sequence 344, App
17	56	100.0	98	1	PCT-US03-00398-344	Sequence 348, App
18	56	100.0	98	1	PCT-US03-00398-348	Sequence 350, App
19	56	100.0	98	1	PCT-US03-00398-350	Sequence 361, App
20	56	100.0	98	1	PCT-US03-00398-361	Sequence 362, App
21	56	100.0	98	1	PCT-US03-00398-362	Sequence 373, App
22	56	100.0	98	1	PCT-US03-00398-373	Sequence 374, App
23	56	100.0	98	1	PCT-US03-00398-374	Sequence 3, Appli
24	56	100.0	98	1	PCT-US03-06598-3	Sequence 31, Appli
25	56	100.0	98	20	US-09-674-752-31	Sequence 45, Appli
26	56	100.0	98	22	US-09-751-181-45	Sequence 27332, A
27	56	100.0	98	22	US-09-791-537-27332	Sequence 77776, A
28	56	100.0	98	22	US-09-791-537-77778	Sequence 45, Appli
29	56	100.0	98	26	US-10-029-526B-45	Sequence 45, Appli
30	56	100.0	98	26	US-10-029-988B-45	Sequence 45, Appli
31	56	100.0	98	26	US-10-032-037B-45	Sequence 45, Appli
32	56	100.0	98	26	US-10-032-423A-45	Sequence 289, App
33	56	100.0	98	26	US-10-041-860-289	Sequence 290, App
34	56	100.0	98	26	US-10-041-860-290	Sequence 235, App
35	56	100.0	98	26	US-10-041-860-295	Sequence 236, App
36	56	100.0	98	26	US-10-041-860-296	Sequence 342, App
37	56	100.0	98	26	US-10-041-860-342	Sequence 344, App
38	56	100.0	98	26	US-10-041-860-344	Sequence 348, App
39	56	100.0	98	26	US-10-041-860-348	Sequence 350, App
40	56	100.0	98	26	US-10-041-860-350	Sequence 361, App
41	56	100.0	98	26	US-10-041-860-361	Sequence 362, App
42	56	100.0	98	26	US-10-041-860-362	Sequence 373, App
43	56	100.0	98	26	US-10-041-860-373	Sequence 374, App
44	56	100.0	98	26	US-10-041-860-374	Sequence 45, Appli
45	56	100.0	98	27	US-10-189-358A-45	

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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234-125

Query Match      100.0%; Score 56; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      1 GYTFTSYDIN 10

RESULT 2
US-10-726-332-125
; Sequence 125, Application US/10726332
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-125

Query Match      100.0%; Score 56; DB 32; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      1 GYTFTSYDIN 10

RESULT 3
PCT-US01-00663-34182
; Sequence 34182, Application PC/TUS0100663
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: PCT/US01/00663
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34182
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUATE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUATE 8.00e-48
PCT-US01-00663-34182

Query Match      100.0%; Score 56; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      17 GYTFTSYDIN 26

RESULT 4
US-09-864-761-47202
; Sequence 47202, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408

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; CURRENT APPLICATION NUMBER: US/10/203,136
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34115
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48
US-10-203-136-34115

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Query Match          100.0%; Score 56; DB 28; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 GYFTSYDIN 10
        |||||
DB      17 GYFTSYDIN 26

```

```

RESULT 8
US-10-203-137-34182
; Sequence 34182, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 34182
; LENGTH: 92

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48
US-10-203-137-34182

```

```

Query Match          100.0%; Score 56; DB 28; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 GYFTSYDIN 10
        |||||
DB      17 GYFTSYDIN 26

```

```

RESULT 9
PCT-US02-22011-3
; Sequence 3, Application PC/TUS0222011
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.02
; CURRENT APPLICATION NUMBER: PCT/US02/22011
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-22011-3

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```

Query Match          100.0%; Score 56; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYFTSYDIN 10
        |||||
DB      24 GYFTSYDIN 33

```

```

RESULT 10
US-10-194-975-3
; Sequence 3, Application US/10194975
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-3

```

```

Query Match          100.0%; Score 56; DB 27; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYFTSYDIN 10

```

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Db      24  GYTFTSYDIN 33
|||||
RESULT 11
PCT-US02-38450-43
; Sequence 43, Application PC/TUS0238450
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: PCT/US02/38450
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
PCT-US02-38450-43

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 12
PCT-US03-00398-289
; Sequence 289, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-289

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 13
PCT-US03-00398-290
; Sequence 290, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-290

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 14
PCT-US03-00398-295
; Sequence 295, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-295

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||

RESULT 15
PCT-US03-00398-296
; Sequence 296, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-296

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GYTFTSYDIN 10
|||||
Db      26  GYTFTSYDIN 35
|||||
```

```

; FILE REFERENCE: AGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-296

Query Match      100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTYDIN 10
Db      26 GYTFSTYDIN 35

Search completed: April 21, 2004, 17:57:21
Job time : 148.696 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:34:09 ; Search time 7.10145 Seconds
(without alignments)
39.310 Million cell updates/sec

Title: SEQ1
Perfect score: 56
Sequence: 1 gytftsytidin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198209 seqs, 2791599 residues

Total number of hits satisfying chosen parameters: 198209

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
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4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	1 PCT-US03-38234A-125	Sequence 125, Appl
2	52	92.9	118	5 US-09-926-323A-2	Sequence 2, Appl
3	51	91.1	127	6 US-10-793-479-4122	Sequence 4122, Ap
4	48	85.7	10	1 PCT-US03-36870-31	Sequence 31, Appl
5	48	85.7	113	1 PCT-US03-36870-3	Sequence 3, Appl
6	48	85.7	113	1 PCT-US03-36870-5	Sequence 5, Appl
7	48	85.7	113	1 PCT-US03-36870-7	Sequence 7, Appl
8	48	85.7	113	1 PCT-US03-36870-8	Sequence 8, Appl
9	48	85.7	113	1 PCT-US03-36870-9	Sequence 9, Appl
10	48	85.7	113	1 PCT-US03-36870-10	Sequence 10, Appl
11	48	85.7	113	1 PCT-US03-36870-11	Sequence 11, Appl
12	47	83.9	116	6 US-10-800-197-120	Sequence 120, App
13	47	83.9	226	6 US-10-813-977-17	Sequence 17, Appl
14	47	83.9	245	6 US-10-800-197-7	Sequence 7, Appl
15	46	82.1	115	6 US-10-488-673-4	Sequence 4, Appl
16	46	82.1	479	1 PCT-US03-34610-12	Sequence 12, Appl
17	45	80.4	149	6 US-10-693-629-56	Sequence 56, Appl
18	44	78.6	109	6 US-10-800-197-147	Sequence 147, App
19	44	78.6	118	6 US-10-789-090-9	Sequence 9, Appl
20	44	78.6	118	6 US-10-803-653-165	Sequence 165, App
21	44	78.6	118	6 US-10-803-622-165	Sequence 165, App
22	44	78.6	120	6 US-10-793-479-4111	Sequence 4111, Ap
23	44	78.6	121	6 US-10-793-479-4115	Sequence 4115, Ap
24	43	76.8	10	1 PCT-US04-05247-6	Sequence 6, Appl
25	43	76.8	10	6 US-10-018-245A-1	Sequence 1, Appl
26	43	76.8	92	6 US-10-681-421-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1

PCT-US03-38234A-125
; Sequence 125, Application PC/TUS0338234A
; GENERAL INFORMATION:
; APPLICANT: AGENIX, INC.
; APPLICANT: LEXICON GENETICS INCORPORATED
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX 072VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38234A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/38234
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234A-125

Query Match 100.0%; Score 56; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYTFTSYDIN 10
Db 1 GYTFTSYDIN 10

RESULT 2

US-09-926-323A-2
; Sequence 2, Application US/09926323A
; GENERAL INFORMATION:
; APPLICANT: Schmitt, Manfred
; APPLICANT: Noack, Frank
; APPLICANT: Magdolen, Viktor
; APPLICANT: Graeff, Henner
; APPLICANT: Luther, Thomas
; APPLICANT: Albrecht, Sybille
; APPLICANT: Muller, Martin
; APPLICANT: Wilhelm, Olaf

Sequence 20, Appl
Sequence 406, App
Sequence 410, App
Sequence 7, Appl
Sequence 31, Appl
Sequence 52, Appl
Sequence 111, App
Sequence 242, App
Sequence 7801, App
Sequence 2, Appl
Sequence 109, App
Sequence 15, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl

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; APPLICANT: Harbeck, Nadia
; TITLE OF INVENTION: Diagnostic and Therapeutic Use of Antibodies Against The
; TITLE OF INVENTION: Urokinase Receptor
; FILE REFERENCE: 2923-508
; CURRENT APPLICATION NUMBER: US/09/926,323A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: PCT/EP00/03347
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.2
; SEQ ID NO 2
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phage sequence
US-09-926-323A-2

Query Match      92.9%; Score 52; DB 5; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYTFSTSYDIN 10
Db      26 GYSFTSYDIN 35

RESULT 3
US-10-793-479-4122
; Sequence 4122, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4122
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
; OTHER INFORMATION: score 9.7
; OTHER INFORMATION: seq ILFLVAATSAHS/QV
US-10-793-479-4122

Query Match      91.1%; Score 51; DB 6; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYTFSTSYDIN 10
Db      45 GYTFVSYDIN 54

RESULT 4
PCT-US03-36870-31
; Sequence 31, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; APPLICANT: Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US03/36870
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 31
PCT-US03-36870-31

Query Match      85.7%; Score 48; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYTFSTSYDIN 10
Db      1 GYTFVNDIH 10

RESULT 5
PCT-US03-36870-3
; Sequence 3, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; APPLICANT: Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US03/36870
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411

```


TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3
PCT-US03-36870-3

Query Match 85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 26 GYTFNYDIH 35

RESULT 6
PCT-US03-36870-5
; Sequence 5, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapero & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 319-5411
TELEFAX: (310) 319-5401

INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5
PCT-US03-36870-5

Query Match 85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 26 GYTFNYDIH 35

RESULT 7
PCT-US03-36870-7

; Sequence 7, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapero & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 319-5411
TELEFAX: (310) 319-5401

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7
PCT-US03-36870-7

Query Match 85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
DB 26 GYTFNYDIH 35

RESULT 8

PCT-US03-36870-8

; Sequence 8, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; Ruben J. Boado
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapero & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003

```

; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8
PCT-US03-36870-8

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTTSYDIN 10
Db      26 GYFTNYDIH 35

RESULT 9
PCT-US03-36870-9
; Sequence 9, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US03/36870
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9
PCT-US03-36870-9

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GYFTTSYDIN 10
Db      26 GYFTNYDIH 35

RESULT 10
PCT-US03-36870-10
; Sequence 10, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US03/36870
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10
PCT-US03-36870-10

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYFTTSYDIN 10
Db      26 GYFTNYDIH 35

RESULT 11
PCT-US03-36870-11
; Sequence 11, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; Via The Human Insulin Receptor
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:

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/
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 2000
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US03/36870
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oldenkamp, David J.
/ REGISTRATION NUMBER: 29,421
/ REFERENCE/DOCKET NUMBER: 0180.0038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (310) 319-5411
/ TELEFAX: (310) 319-5401
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 12
US-10-800-197-120
; Sequence 120, Application US/10800197
; GENERAL INFORMATION:
; APPLICANT: Morton, Philip A et al.
; TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 01343/1
; CURRENT APPLICATION NUMBER: US/10/800,197
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/455,094
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 120
; LENGTH: 116
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: phage display generated VH or VL region
US-10-800-197-120

Query Match      83.9%; Score 47; DB 6; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 13
US-10-813-977-17
; Sequence 17, Application US/10813977
; GENERAL INFORMATION:
; APPLICANT: Dyanan, William
; APPLICANT: Takeda, Yoshihiko
; APPLICANT: Li, Shuyi
; TITLE OF INVENTION: Compositions and Methods for Modulating DNA Repair
; FILE REFERENCE: 791301-1010

/
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 2000
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US03/36870
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oldenkamp, David J.
/ REGISTRATION NUMBER: 29,421
/ REFERENCE/DOCKET NUMBER: 0180.0038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (310) 319-5411
/ TELEFAX: (310) 319-5401
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 12
US-10-800-197-120
; Sequence 120, Application US/10800197
; GENERAL INFORMATION:
; APPLICANT: Morton, Philip A et al.
; TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 01343/1
; CURRENT APPLICATION NUMBER: US/10/800,197
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/455,094
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 120
; LENGTH: 116
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: phage display generated VH or VL region
US-10-800-197-120

Query Match      83.9%; Score 47; DB 6; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 13
US-10-813-977-17
; Sequence 17, Application US/10813977
; GENERAL INFORMATION:
; APPLICANT: Dyanan, William
; APPLICANT: Takeda, Yoshihiko
; APPLICANT: Li, Shuyi
; TITLE OF INVENTION: Compositions and Methods for Modulating DNA Repair
; FILE REFERENCE: 791301-1010

/
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 2000
/ SOFTWARE: MS Word
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US03/36870
/ FILING DATE: 18-Nov-2003
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oldenkamp, David J.
/ REGISTRATION NUMBER: 29,421
/ REFERENCE/DOCKET NUMBER: 0180.0038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (310) 319-5411
/ TELEFAX: (310) 319-5401
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11

Query Match      85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 12
US-10-800-197-120
; Sequence 120, Application US/10800197
; GENERAL INFORMATION:
; APPLICANT: Morton, Philip A et al.
; TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 01343/1
; CURRENT APPLICATION NUMBER: US/10/800,197
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/455,094
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 120
; LENGTH: 116
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: phage display generated antibody
US-10-800-197-7

Query Match      83.9%; Score 47; DB 6; Length 245;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GYTFSTSYDIN 10
Db      26 GYTFNYDIH 35

RESULT 15
US-10-488-673-4
; Sequence 4, Application US/10488673
; GENERAL INFORMATION:
; APPLICANT: KEIO UNIVERSITY
; TITLE OF INVENTION: PEMPHIGUS MONOCLONAL ANTIBODIES
; FILE REFERENCE: P10000238
; CURRENT APPLICATION NUMBER: US/10/488,673
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: JP P2001-267653
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-488-673-4

Query Match      82.1%; Score 46; DB 6; Length 115;
Best Local Similarity 90.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
```

Qy 1 GYFTSYDIN 10
|||
Db 26 GYFTSYWIN 35
|||

Search completed: April 21, 2004, 17:58:24
Job time : 8.10145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 40 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gyftsydin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	92	4	AAM20077 Peptide #
2	56	100.0	92	4	AAM33913 Peptide #
3	56	100.0	92	4	ABG55467 Human liv
4	56	100.0	92	5	ABG43604 Human pep
5	56	100.0	98	3	AAY50958 Human FVI
6	56	100.0	98	5	ABG78170 Human Fv
7	56	100.0	98	5	ABG31861 Human ant
8	56	100.0	98	6	ABO27070 Human ger
9	56	100.0	116	2	AAR79241 Heavy cha
10	56	100.0	117	2	AAR66302 Human imm
11	56	100.0	119	6	ABJ18572 Ganglios
12	56	100.0	119	6	ABJ18570 Ganglios
13	56	100.0	120	4	AAB62747 Human HIV
14	56	100.0	122	6	ABR55829 Heavy cha
15	56	100.0	139	6	ABG74245 Mouse ant
16	56	100.0	146	3	AAB53510 Human col
17	56	100.0	149	6	ABO04846 Human epi
18	56	100.0	199	2	AAY34302 IGM antib
19	56	100.0	203	2	AAY34301 IGM antib
20	56	100.0	555	4	AAB19871 Activatin
21	56	100.0	565	4	AAB19873 Activatin
22	56	100.0	577	4	AAB19872 Activatin
23	56	100.0	704	4	AAB19888 MLV envel
24	54	96.4	120	6	ABR55815 Heavy cha
25	53	94.6	120	6	AAO29544 Human 7.1

26	53	94.6	120	6	ABG71906 Human ant
27	53	94.6	243	7	ABM78999 Monoclonona
28	53	94.6	243	7	ABM78998 Monoclonona
29	52	92.9	118	3	ABE11391 Murine II
30	52	92.9	123	4	AAU02552 Anti-adip
31	51	91.1	119	5	ABO07175 Mouse 09
32	51	91.1	127	3	AAG00041 Human sec
33	51	91.1	134	3	AAY64688 Human 5,
34	51	91.1	850	4	ABG04634 Novel hum
35	50	89.3	122	3	AAY50959 Human FVI
36	50	89.3	122	3	AAY50966 Human FVI
37	50	89.3	476	2	AAW88464 Monoclonona
38	49	87.5	127	4	AAU02622 Anti-adip
39	49	87.5	248	5	ABP44997 Human Bly
40	49	87.5	561	2	AAY17415 Mouse imm
41	48	85.7	10	3	AAY78322 Anti-zeta
42	48	85.7	115	2	AAR52051 Heavy cha
43	48	85.7	123	3	AAY78325 Anti-zeta
44	48	85.7	268	2	AAK44226 Chlmeric
45	48	85.7	532	3	AAY78328 Bispecific

ALIGNMENTS

RESULT 1

AAW20077
ID AAM20077 standard; protein; 92 AA.

XX
AC AAM20077;

XX
DT 12-OCT-2001 (first entry)

XX
DE Peptide #511 encoded by probe for measuring cervical gene expression.

XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;

XX
KW cervical cancer.

XX
OS Homo sapiens.

XX
PN WO200157278-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000670.

XX
PR 04-FEB-2000; 2000US-0180312P.

XX
PR 26-MAY-2000; 2000US-0207456P.

XX
PR 30-JUN-2000; 2000US-00608408.

XX
PR 03-AUG-2000; 2000US-00632366.

XX
PR 21-SEP-2000; 2000US-0234687P.

XX
PR 27-SEP-2000; 2000US-0236359P.

XX
PR 04-OCT-2000; 2000GB-00024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
WPI; 2001-488901/53.

XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX
PS Gene expression in human cervical epithelial cells.

XX
CC Claim 27; SEQ ID NO 24903; 487pp; English.

XX
CC The present invention relates to human single exon nucleic acid probes
(SENP; see AAI10068-AA128459). The present sequence is a peptide encoded
by one such probe. The SENPs are derived from human HeLa cells. The SENPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer. Note: The sequence data for this patent did not form

```
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 92 AA;
  Query Match      100.0%; Score 56; DB 4; Length 92;
  Best Local Similarity 100.0%; Pred. No. 0.06;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
Db 17 GYTFSTSYDIN 26

RESULT 2
ID AAM33913 standard; protein; 92 AA.
XX
AC AAM33913;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #7950 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW Genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 34182; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AA31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 92 AA;
  Query Match      100.0%; Score 56; DB 4; Length 92;
  Best Local Similarity 100.0%; Pred. No. 0.06;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
Db 17 GYTFSTSYDIN 26

RESULT 3
```

```
ABG55467
ID ABG55467 standard; peptide; 92 AA.
XX
AC ABG55467;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 34115.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 34115; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 92 AA;
  Query Match      100.0%; Score 56; DB 4; Length 92;
  Best Local Similarity 100.0%; Pred. No. 0.06;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
Db 17 GYTFSTSYDIN 26

RESULT 4
ID ABG43604 standard; peptide; 92 AA.
XX
AC ABG43604;
XX
DT 19-AUG-2002 (first entry)
XX
```

DE Human peptide encoded by genome-derived single exon probe SEQ ID 33269.
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX Homo sapiens.
 OS
 XX
 XX WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234587P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 XX Claim 27; SEQ ID NO 33269; 634pp; English.
 XX
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 92 AA;
 Query Match 100.0%; Score 56; DB 5; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYTFSTYDIN 10
 DB 17 GYTFSTYDIN 26
 RESULT 5
 AAY50958
 ID AAY50958 standard; protein; 98 AA.
 XX
 AC AAY50958;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
 XX
 KW Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A;
 KW scFv; A3-C1.
 XX
 OS Homo sapiens.
 XX
 PN WO9958680-A2.
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-NL000285.
 XX
 PR 08-MAY-1998; 98EP-00201543.
 XX
 PR (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
 PA Voorberg JJ, Van Den Brink EN, Turenhout EM;
 PI WPI; 2000-053102/04.
 XX
 XX New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for treatment
 PT of hemophilia A patients with these antibodies.
 XX
 PS Example 8; Fig 9A; 61pp; English.
 XX
 XX This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specificity which has
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them are
 CC useful in compositions for neutralizing factor VIII inhibiting antibodies
 CC in hemophilia A patients. This sequence represents the human factor VIII
 CC antibody A3-C1 specific scFv protein DP-15 which is used in the method of
 CC the invention
 XX
 XX Sequence 98 AA;
 Query Match 100.0%; Score 56; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYTFSTYDIN 10
 DB 26 GYTFSTYDIN 35

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RESULT 6
ABG78170
ID ABG78170 standard; protein; 98 AA.
XX
AC ABG78170;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Fv molecule hypervariable region related peptide #45.
XX
KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS Homo sapiens.
XX
PN WO200259264-A2.
XX
PD 01-AUG-2002.
XX
PF 31-DEC-2001; 2001WO-US049440.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
XX
DR WPI; 2002-619166/66.
XX
PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Claim 13; Page 168-169; 232pp; English.
XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 56; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. NO. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
Db 26 GYTFSTSYDIN 35

RESULT 7
ABG91861
ID ABG91861 standard; protein; 98 AA.
XX
AC ABG91861;
XX
DT 04-DEC-2002 (first entry)
XX

```

```

DE Human antibody fragment #45.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 246; Opp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 56; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. NO. 0.064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSTSYDIN 10
Db 26 GYTFSTSYDIN 35

RESULT 8
ABO27070
ID ABO27070 standard; protein; 98 AA.
XX
AC ABO27070;
XX
DT 10-SEP-2003 (first entry)
XX

```



```

XX DE Human germline heavy chain variable region gene segment #3.
XX OS
XX KW Human; heavy chain variable region; VH; humanised antibody;
XX KW chimeric antibody; complementarity determining region; CDR;
XX KW canonical CDR structure type.
XX OS
XX OS Homo sapiens.
XX XX
XX PN US2003039649-A1.
XX PD 27-FEB-2003.
XX XX
XX PF 12-JUL-2002; 2002US-00194975.
XX XX
XX PR 12-JUL-2001; 2001US-0305111P.
XX XX
XX PA (FOOT/) FOOTE J.
XX XX
XX PI Foote J;
XX DR WPI; 2003-492151/46.
XX XX
XX PT Making humanized antibody for converting antibody, by making chimeric
XX PT antibodies containing complementarity determining region from non-human
XX PT antibody and appropriate framework sequences of human antibodies.
XX PS
XX PS Example 1; Fig 1; 3lpp; English.
XX CC
XX CC The invention describes a method of making a humanised antibody,
XX CC comprising making chimeric antibodies containing a complementarity
XX CC determining region (CDR) from a non-human antibody and appropriate
XX CC framework sequences (I) of human antibodies. (I) is selected by using
XX CC canonical CDR structure types of non-human antibody in comparison to
XX CC germline canonical CDR structure types of human antibodies as the basis
XX CC for selection, for humanisation. The method is useful for making a
XX CC humanised antibody or a converted antibody. The method is applicable for
XX CC converting a subject antibody sequence of any subject species to a less
XX CC immunogenic form suitable for use in an object species. The method is
XX CC reliable for identifying suitable human framework sequences to support
XX CC non-human CDR regions and to provide humanised antibodies that retain
XX CC high antigen binding with low immunogenicity in humans without the need
XX CC for direct comparison of framework sequences, without the need for
XX CC determining critically important amino acid residues in the framework,
XX CC and without the need for multiple iteration and construction to obtain
XX CC humanised antibodies with suitable therapeutic properties. The antibody
XX CC has high affinity and low immunogenicity without need for comparing
XX CC framework sequences between non-human and human antibodies. This sequence
XX CC represents a human heavy chain variable region gene segment used in the
XX CC creation of humanised antibodies
XX SQ
XX SQ Sequence 98 AA;
XX Query Match 100.0%; Score 56; DB 6; Length 98;
XX Best Local Similarity 100.0%; Pred. No. 0.064;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYTFSTSYDIN 10
XX | | | | |
XX Db 26 GYTFSTSYDIN 35
XX
XX RESULT 9
XX ID AAR79241
XX AC AAR79241 standard; protein; 116 AA.
XX XX
XX AC AAR79241;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 21-DEC-1995 (first entry)
XX XX
XX DE Heavy chain variable region for monoclonal antibody 4A10.
XX KW
XX KW cosmid; placenta; vector; pJB81; E.coli; mammalian.

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KW XX Monoclonal antibody; heavy metal; mercury; variable region; heavy chain.
XX OS
XX OS Synthetic.
XX PN WO9520607-A1.
XX PD 03-AUG-1995.
XX XX
XX PF 27-JAN-1995; 95WO-US001199.
XX XX
XX PR 27-JAN-1994; 94US-00187407.
XX XX
XX PA (BION-) BIONEERASKA INC.
XX XX
XX PI Lopez O, Wylie DE, Wagner F;
XX XX
XX DR WPI; 1995-275415/36.
XX DR N-PSDB; AAQ97498.
XX XX
XX PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
XX PT monoclonal antibodies, used for detecting, removing, adding or
XX PT neutralising heavy metals.
XX PS
XX PS Claim 13; Page 54; 106pp; English.
XX XX
XX XX Hybridoma antibodies have been produced with the spleen cells of BALB/c
XX CC mouse that had received multiple injections of mercuric ions reacted with
XX CC glutathione to produce a mercuric ion coordinate covalent compound which
XX CC was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas
XX CC (1F10, 4A10, 1C11, 5G4, 23F8, 2D5, 5B6 and 3E8) were producing MAbs that
XX CC against glutathione without mercuric ions. RNA was isolated from
XX CC hybridoma cells with guanidine isothiocyanate. First strand cDNA
XX CC synthesis was catalysed by MuLV reverse transcriptase. The primers used
XX CC for cDNA synthesis were complementary to the 5' end of the CH1 domain of
XX CC the heavy chain expressed by the hybridoma of interest, or to the 5' and
XX CC the C kappa domain. Some of the primers used for cDNA synthesis are
XX CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
XX CC variable region of a particular antibody polypeptide was also used for
XX CC PCR amplification of that variable region, in conjunction with an
XX CC appropriate V-region primer. In addition, the VH primer AAQ97518 was used
XX CC to amplify the mAb 2D5 and 5B6 heavy chains. The sequences of the PCR
XX CC amplified nucleotides were determined. These are given in AAQ97498-Q97510
XX CC and the deduced AA sequences in AAR79241-R9250 & AAR78970-R78971. The
XX CC descriptions of the SEQ ID nos given on pp 44-45 and in the claims are
XX CC different from the descriptions in the sequence listings. The
XX CC descriptions in the sequence listings are used here. (Updated on 25-MAR-
XX CC 2003 to correct FN field.)
XX SQ
XX SQ Sequence 116 AA;
XX Query Match 100.0%; Score 56; DB 2; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 0.076;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYTFSTSYDIN 10
XX | | | | |
XX Db 26 GYTFSTSYDIN 35
XX
XX RESULT 10
XX ID AAR66302
XX AC AAR66302 standard; protein; 117 AA.
XX XX
XX AC AAR66302;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 02-AUG-1995 (first entry)
XX XX
XX DE Human immunoglobulin variable heavy chain #8.
XX XX
XX XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
XX KW cosmid; placenta; vector; pJB81; E.coli; mammalian.

```

```

XX OS Homo sapiens.
XX PN WO9426895-A1.
XX PD 24-NOV-1994.
XX PF 10-MAY-1993; 93WO-JP000603.
XX PR 10-MAY-1993; 93WO-JP000603.
XX PA (NIBS ) JAPAN TOBACCO INC.
XX PI Honjo T, Matsuda F;
XX DR WPI; 1995-006791/01.
XX DR N-PSDB; AAQ78946.
XX PT DNA fragment comprising human immunoglobulin Vh genes - for the
XX PS production of human immunoglobulin in mammalian hosts.
XX PS Claim 17; Page 41-42; 130pp; Japanese.
XX CC Protein sequences (AAR6295-51) are novel human immunoglobulin heavy
XX CC chain sequences encoded by novel isolated genes. The genes (AAQ78939-
XX CC 79002) were isolated and cloned from a series of cosmid constructs: Y202;
XX CC Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using
XX CC primers AAQ78917-38. The genes are subdivided into 5 families of Vh
XX CC genes. The fragments cover a region of 800 kb. The DNA fragments were
XX CC isolated from high molecular weight DNA from human placenta. The DNA was
XX CC partially digested with Taqi restriction enzyme. The fragments were
XX CC separated by gel electrophoresis and 35-45 kb fractions were collected.
XX CC The fragments were ligated with ClaI-digested cosmid vector pJB81. The
XX CC ligation products were in vitro packed and infected into E.coli 490A. The
XX CC fragments were then subcloned by colony hybridisation. The Vh genes and
XX CC the DNA fragments encoding them are useful in producing human
XX CC immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 117 AA;
    Query Match 100.0%; Score 56; DB 2; Length 117;
    Best Local Similarity 100.0%; Pred. No. 0.076;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 45 GYTFTSYDIN 54

RESULT 11
ABJ18572
XX AC ABJ18572;
XX DT 18-FEB-2003 (first entry)
XX DE Ganglioside-associated recombinant antibody related VHLE10 protein #2.
XX KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
XX KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
XX KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
XX KW sarcoma; neuroectodermal.
XX OS Unidentified.
XX PN WO200281496-A2.
XX PD 17-OCT-2002.
XX PF 08-APR-2002; 2002WO-CU000003.
XX PR 06-APR-2001; 2001CU-00000084.
XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
XX PA (VALL/) LOMBARDERO VALLADARES J.
XX PA (NAVA/) ROQUE NAVARRO L T.
XX PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
XX PI Roque Navarro LT, Lopez Requena A;

QY 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35

RESULT 12
ABJ18570
XX ID ABJ18570 standard; protein; 119 AA.
XX AC ABJ18570;
XX DT 18-FEB-2003 (first entry)
XX DE Ganglioside-associated recombinant antibody related VH 1E10 protein.
XX KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
XX KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
XX KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
XX KW sarcoma; neuroectodermal.
XX OS Unidentified.
XX PN WO200281496-A2.
XX PD 17-OCT-2002.
XX PF 08-APR-2002; 2002WO-CU000003.
XX PR 06-APR-2001; 2001CU-00000084.
XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
XX PA (VALL/) LOMBARDERO VALLADARES J.
XX PA (NAVA/) ROQUE NAVARRO L T.
XX PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
XX PI Roque Navarro LT, Lopez Requena A;

PR 06-APR-2001; 2001CU-00000084.
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
XX PA (VALL/) LOMBARDERO VALLADARES J.
XX PA (NAVA/) ROQUE NAVARRO L T.
XX PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
XX PI Roque Navarro LT, Lopez Requena A;

XX WPI; 2003-046957/04.
XX New chimeric antibodies, useful for treatment, prevention and diagnosis
XX PT of tumors that express gangliosides, are derived from monoclonal
XX PT antibodies P3 or 1E10.
XX PS Example 6; Fig 8; 31pp; Spanish.
XX CC The invention relates to a chimeric antibody, derived from a monoclonal
XX CC antibody, which recognises N-glycosylated gangliosides and is produced by
XX CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
XX CC derived from the anti-idiotypic monoclonal 1E10 (recognising P3) are used
XX CC for treatment, localisation and in vivo identification of breast cancer
XX CC and melanoma, their metastases and relapses, tumours of lung, digestive
XX CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
XX CC This sequence represents a protein relating to the chimeric antibody of
XX CC the invention
XX SQ Sequence 119 AA;
    Query Match 100.0%; Score 56; DB 6; Length 119;
    Best Local Similarity 100.0%; Pred. No. 0.078;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35

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Best Local Similarity 100.0%; Pred. No. 0.079;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 21, 2004, 17:33:09

Job time : 42 secs

QY 1 GYTFTSYDIN 10

Db 26 GYTFTSYDIN 35

RESULT 15

ABG74245

ID ABG74245 standard; protein; 139 AA.

XX AC ABG74245;

DT 22-APR-2003 (first entry)

XX DE Mouse antibody 4D4 heavy chain variable region.

XX KW T-cell receptor; cytostatic; dermatological; neuroprotective;

XX KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

XX KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

XX KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

XX KW small cell lung cancer; heavy chain variable region; mouse.

XX OS Mus sp.

XX PN US2002132983-A1.

XX PD 19-SEP-2002.

XX PF 10-DEC-2001; 2001US-00006773.

XX PR 30-NOV-2000; 2000US-0250087P.

XX PR 30-NOV-2000; 2000US-0250089P.

XX PA (JUNG/) JUNGHANS R P.

XX PI Junghans RP;

XX DR WPI; 2003-208946/20.

XX DR N-PSDB; ABX16571.

XX PT New chimeric molecule useful in treating patients with disorders, such as

XX PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer

XX PT comprises GD3 and/or PSMA binding domains of antibody.

XX PS Disclosure; Page 14-15; 35pp; English.

XX CC The invention relates to a chimaeric molecule comprising the GD3

XX CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

XX CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)

XX CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

XX CC sequences, the zeta signalling chain of the T cell receptor and an

XX CC intervening CD8alpha hinge in which cysteine residues have been mutated.

XX CC The chimaeric molecules expressed in T cells or NK cells or other

XX CC effector cells are useful in treating patients with cancers expressing

XX CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

XX CC and/or together with each other or with heterologous constructs to engage

XX CC additional stimulatory and functional properties of the effector cells to

XX CC enhance the antitumour therapeutic efficacy (claimed). They are

XX CC particularly useful in disorders including melanoma, neuroendocrine

XX CC tumours and prostate and small cell lung cancer. The present sequence

XX CC represents the mouse antibody 4D4 heavy chain variable region

XX SQ Sequence 139 AA;

Query Match 100.0%; Score 56; DB 6; Length 139;

Best Local Similarity 100.0%; Pred. No. 0.09;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10

Db 45 GYTFTSYDIN 54

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 30.1449 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gyvftsydin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	92	9	US-09-864-761-47202
2	56	100.0	96	14	US-10-194-975-3
3	56	100.0	98	12	US-10-453-698-43
4	56	100.0	98	12	US-10-029-926B-45
5	56	100.0	98	14	US-10-041-860-289
6	56	100.0	98	14	US-10-041-860-290
7	56	100.0	98	14	US-10-041-860-295
8	56	100.0	98	14	US-10-041-860-296
9	56	100.0	98	14	US-10-041-860-342
10	56	100.0	98	14	US-10-041-860-344
11	56	100.0	98	14	US-10-041-860-348
12	56	100.0	98	14	US-10-041-860-350
13	56	100.0	98	14	US-10-041-860-361
14	56	100.0	98	14	US-10-041-860-362
15	56	100.0	98	14	US-10-041-860-373

ALIGNMENTS

RESULT 1

- US-09-864-761-47202
- Sequence 47202, Application US/09864761
- Patent No. US20020048763A1
- GENERAL INFORMATION:
- APPLICANT: Penn, Sharron G.
- APPLICANT: Rank, David R.
- APPLICANT: Hanzel, David K.
- APPLICANT: Chen, Weisheng
- TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
- TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
- FILE REFERENCE: Aescmca-X-1
- CURRENT APPLICATION NUMBER: US/09/864.761
- CURRENT FILING DATE: 2001-05-23
- PRIOR APPLICATION NUMBER: US 60/180,312
- PRIOR FILING DATE: 2000-02-04
- PRIOR APPLICATION NUMBER: US 60/207,456
- PRIOR FILING DATE: 2000-05-26
- PRIOR APPLICATION NUMBER: US 09/632,366
- PRIOR FILING DATE: 2000-08-03
- PRIOR APPLICATION NUMBER: GB 24263.6
- PRIOR FILING DATE: 2000-10-04
- PRIOR APPLICATION NUMBER: US 60/236,359
- PRIOR FILING DATE: 2000-09-27
- PRIOR APPLICATION NUMBER: PCT/US01/00666
- PRIOR FILING DATE: 2001-01-30
- PRIOR APPLICATION NUMBER: PCT/US01/00667
- PRIOR FILING DATE: 2001-01-30
- PRIOR APPLICATION NUMBER: PCT/US01/00664
- PRIOR FILING DATE: 2001-01-30
- PRIOR APPLICATION NUMBER: PCT/US01/00669
- PRIOR FILING DATE: 2001-01-30
- PRIOR APPLICATION NUMBER: PCT/US01/00665
- PRIOR FILING DATE: 2001-01-30
- PRIOR APPLICATION NUMBER: PCT/US01/00668
- PRIOR FILING DATE: 2001-01-30
- PRIOR APPLICATION NUMBER: PCT/US01/00663
- PRIOR FILING DATE: 2001-01-30

- Sequence 374, Appl
- Sequence 43, Appl
- Sequence 45, Appl
- Sequence 45, Appl
- Sequence 45, Appl
- Sequence 1, Appl
- Sequence 61, Appl
- Sequence 38, Appl
- Sequence 48, Appl
- Sequence 200, Appl
- Sequence 203, Appl
- Sequence 237, Appl
- Sequence 238, Appl
- Sequence 240, Appl
- Sequence 343, Appl
- Sequence 372, Appl
- Sequence 19, Appl
- Sequence 21, Appl
- Sequence 199, Appl
- Sequence 201, Appl
- Sequence 236, Appl
- Sequence 268, Appl
- Sequence 294, Appl
- Sequence 44, Appl
- Sequence 205, Appl
- Sequence 242, Appl
- Sequence 360, Appl
- Sequence 31, Appl
- Sequence 67, Appl
- Sequence 13, Appl

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47202
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUATE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUATE 8.00e-48
US-09-864-761-47202
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Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
Db 17 GYTFTSYDIN 26
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RESULT 2

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US-10-194-975-3
; Sequence 3, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-3
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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
Db 24 GYTFTSYDIN 33
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RESULT 3

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US-10-453-698-43
; Sequence 43, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
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; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-453-698-43
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Query Match 100.0%; Score 56; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35
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RESULT 4

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US-10-029-926B-45
; Sequence 45, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-45
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Query Match 100.0%; Score 56; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GYTFTSYDIN 10
Db 26 GYTFTSYDIN 35
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RESULT 5

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US-10-041-860-289
; Sequence 289, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiac-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyan
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
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US-10-041-860-299

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Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 26 GYTFTSYDIN 35

RESULT 6

US-10-041-860-290
; Sequence 290, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-290

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 26 GYTFTSYDIN 35

RESULT 7

US-10-041-860-295
; Sequence 295, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-295

Query Match 100.0%; Score 56; DB 14; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYTFTSYDIN 10
DB 26 GYTFTSYDIN 35

RESULT 8

US-10-041-860-296
; Sequence 296, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-296

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
DB 26 GYTFTSYDIN 35

RESULT 9

US-10-041-860-342
; Sequence 342, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-342

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 10
 US-10-041-860-344
 ; Sequence 344, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 344
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-344

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 11
 US-10-041-860-348
 ; Sequence 348, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 348
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-348

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 12
 US-10-041-860-350
 ; Sequence 350, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 350
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; NAME/KEY: VARIANT
 ; LOCATION: 55
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 55
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-041-860-350

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
 |||||
 Db 26 GYTFTSYDIN 35

RESULT 13
 US-10-041-860-361
 ; Sequence 361, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 361
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-361

Query Match 100.0%; Score 56; DB 14; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.03;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTSYDIN 10

Db 26 GYTFTSYDIN 35

RESULT 14

US-10-041-860-362
; Sequence 362, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 57
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 57
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-362

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTSYDIN 10

Db 26 GYTFTSYDIN 35

RESULT 15

US-10-041-860-373
; Sequence 373, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 98
; TYPE: PRT

; ORGANISM: homo sapiens
US-10-041-860-373

Query Match 100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYTFTSYDIN 10

Db 26 GYTFTSYDIN 35

Search completed: April 21, 2004, 18:02:05
Job time : 31.1449 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 7.6087 seconds
(without alignments)

102.653 Million cell updates/sec

Title: SEQ2

Perfect score: 82

Sequence: 1 inpsngntdyackfq 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	86.6	117	1	HV1G HUMAN
2	62	75.6	117	1	HV1B HUMAN
3	62	75.6	147	1	HV1C HUMAN
4	57	69.5	117	1	HV12 MOUSE
5	57	69.5	117	1	HV13 MOUSE
6	57	69.5	118	1	HV51 MOUSE
7	51	62.2	117	1	HV09 MOUSE
8	51	62.2	117	1	HV10 MOUSE
9	51	62.2	117	1	HV49 MOUSE
10	51	62.2	139	1	HV07 MOUSE
11	50	61.0	120	1	HV50 MOUSE
12	50	61.0	138	1	HV48 MOUSE
13	49	59.8	117	1	HV04 MOUSE
14	45	54.9	120	1	HV03 MOUSE
15	45	54.9	137	1	HV11 MOUSE
16	42	51.2	117	1	HV06 MOUSE
17	42	51.2	136	1	HV15 MOUSE
18	41	50.0	140	1	HV02 MOUSE
19	40	48.8	117	1	HV14 MOUSE
20	40	48.8	117	1	HV1A HUMAN
21	40	48.8	518	1	GSH1_BUCAP
22	40	48.8	1068	1	YCF0_MARPO
23	40	48.8	3329	1	BRC2_MOUSE
24	39	47.6	114	1	HV00 MOUSE
25	39	47.6	117	1	HV52 MOUSE
26	39	47.6	202	1	WR59_ARATH
27	39	47.6	323	1	FMT_CANSP
28	39	47.6	374	1	YMBQ_YEAST
29	39	47.6	398	1	AAAD_HUMAN
30	39	47.6	504	1	Y795_METJA
31	39	47.6	546	1	PGM1_ECOLI
32	39	47.6	566	1	GUNG_CLOTM
33	39	47.6	887	1	NED4_MOUSE

34	39	47.6	887	1	NED4 RAT
35	39	47.6	1000	1	NED4_HUMAN
36	38.5	47.0	295	1	YB45_PYREFU
37	38.5	47.0	1257	1	CAME_HUMAN
38	38	46.3	279	1	YB49_STRP3
39	38	46.3	279	1	YE93_STRPY
40	38	46.3	352	1	STSY_CATRO
41	38	46.3	2164	1	HGAI_PORGI
42	38	46.3	2628	1	HGA2_PORGI
43	37	45.1	124	1	TOXK_WILSA
44	37	45.1	128	1	LYCI_PIG
45	37	45.1	140	1	ATPE_YERPE

ALIGNMENTS

RESULT 1

HV1G_HUMAN STANDARD; PRT; 117 AA.

AC P23083;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region V35 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88296409; PubMed=2841108;

RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,

RA Ohno H., Fukuhara S., Honjo T.;

RT "Dispersed localization of D segments in the human immunoglobulin

RT heavy-chain locus."

RL EMBO J. 7:1047-1051(1988).

CC - SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; X07448; -; NOT_ANNOTATED_CDS.

DR PIR; S00476; HVH035.

DR HSSP; P01772; 2PB4.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.

FT DOMAIN 20 >117 IG-LIKE.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 13009 MW; BE51CE63F8CE97BD CRC64;

Query Match

Best Local Similarity 86.6%; Score 71; DB 1; Length 117;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYACKFQ 15

|||||:|||||

Db 70 INPNSGGTNYACKFQ 84

```

RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RL immunoglobulin epsilon chain expressed in a myeloma cell line.";
RN Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; 1MCP.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; P:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
KW SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
FT SEQUENCE 147 AA; 16491 MW; 949F9F72A5366C20 CRC64;

Query Match 75.6%; Score 62; DB 1; Length 147;
Best Local Similarity 73.3%; Pred. No. 0.0014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
Db |||||:|:|:|:|
70 INPNSGNTDYAOKFQ 84

RESULT 4
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 1045.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RL heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC DR PIR; A02039; MEMS4E.
CC DR HSSP; P01789; 1MCP.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; IGV; 1.
CC DR SMART; SM00406; IGV; 1.

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entities requires a license agreement (See http://www.isb-sib.ch/announcements/
or send an email to license@isb-sib.ch).

EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUG.
DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 75.6%; Score 62; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0011;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
Db |||||:|:|:|:|
70 INPNSGNTDYAOKFQ 84

RESULT 3
HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

```

DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
Query Match 69.5%; Score 57; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.0078; 3; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65
RESULT 5
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN [1]
RP SEQUENCE
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 232E2AF4BE447E41 CRC64;
Query Match 69.5%; Score 57; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.0078; 3; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65
RESULT 6
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN [1]
RP SEQUENCE
RX MEDLINE=84183519; PubMed=5201362;
RA Didrop R., Bovens J., Sikevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
Query Match 69.5%; Score 57; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 0.0079; 3; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNNGGTSYNQKFK 65
RESULT 7
ID HV09 MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; D90809; HVMS61.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117

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SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;
Query Match 62.2%; Score 51; DB 1; Length 117;
Best Local Similarity 60.0%; Pred.No. 0.083;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFQ 15
DB 70 IDPNSGGTKYNEKFK 84

RESULT 8
HV10 MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=C57BL/6;
RX Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
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CC -----
CC EMBL; J00533; AAA38602.1; -.
DR PIR; C90809; HVMS45.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 145.
FT CHAIN 20 117 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 117;
Best Local Similarity 60.0%; Pred.No. 0.083;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFQ 15
DB 70 IDPNSGGTKYNEKFK 84
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RESULT 9
HV49 MOUSE
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Vancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
CC EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION VH558 B4.
FT CHAIN 20 117 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 117;
Best Local Similarity 60.0%; Pred.No. 0.083;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFQ 15
DB 70 IDPNSGGTKYNEKFK 84

RESULT 10
HV07 MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region BI-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
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RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RA "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MENA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL: J00529; AAA38170.1; -.
CC PIR: A90809; MHMS18.
CC PDB: 1A6U; 27-MAY-98.
CC PDB: 1A6W; 15-JUL-98.
CC InterPro: IPR007110; Ig-like.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Signal; 3D-structure.
CC SIGNAL 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 20 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 55 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 139 139
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC0CF465 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 139;
Best Local Similarity 60.0%; Pred. No. 0.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 IDPNSGGTKYNEKFK 84

RESULT 11
HV50 MOUSE
ID HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX SEQUENCE.
EX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
CC PIR: A02037; MHMS15.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003596; IG_V.
CC Pfam: PF00047; Ig; 1.

Query Match 61.0%; Score 50; DB 1; Length 138;
Best Local Similarity 53.3%; Pred. No. 0.15;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 INPNSGNTDYAQKFQ 84

RESULT 12
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P0380;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX SEQUENCE FROM N.A.
RP MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner P.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
CC PIR: A02033; HVMST7.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003596; IG_V.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 20
CC CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
CC DOMAIN 21 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 88 FRAMEWORK-2.
CC DOMAIN 69 95 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 128 138 FRAMEWORK-4.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 138 138
CC SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 61.0%; Score 50; DB 1; Length 138;
Best Local Similarity 53.3%; Pred. No. 0.15;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 70 INPNSGNTDYAQKFQ 84

RESULT 13
HV04 MOUSE
ID HV04 MOUSE STANDARD; PRT; 117 AA.
AC P01748;
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DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain v region 23 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
DR PIR; A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 59.8%; Score 49; DB 1; Length 117;
Best Local Similarity 53.3%; Pred. No. 0.18;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFQ 15
DB 70 INPFGNGTYNKEFK 84

RESULT 14
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain v region 36-65.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.

InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN 1 111 IG-LIKE.
NON_TER 120 120
SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 54.9%; Score 45; DB 1; Length 120;
Best Local Similarity 53.3%; Pred. No. 0.91;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFQ 15
DB 50 INPFGNGTYNKEFK 64

RESULT 15
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain v region 543 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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EMBL; J00539; AAA38172.1; -.
PIR; A02038; G2MS43.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
CHAIN 1 19 IG HEAVY CHAIN V REGION S43.
DOMAIN 20 137 FRAMEWORK-1.
DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
DOMAIN 50 54 FRAMEWORK-2.
DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.
DOMAIN 69 85 FRAMEWORK-3.
DOMAIN 86 117 D SEGMENT.
DOMAIN 118 122 JH2 SEGMENT.
DOMAIN 123 137 BY SIMILARITY.
DISULFID 41 115
NON_TER 137 137
SEQUENCE 137 AA; 15200 MW; ADD5681BF44B8EC9 CRC64;

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Query Match 54.9%; Score 45; DB 1; Length 137;
 Best Local Similarity 53.3%; Pred. No. 1.1;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFPQ 15
 |:|||||:|:
 Db 70 IDPNSGGTTYNEHFR 84

Search completed: April 21, 2004, 17:33:57
 Job time : 8.6087 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 12.029 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ1

Perfect score: 56

Sequence: 1 gyftsydin 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	56	100.0	116	2	US-08-888-366-2		Sequence 2, Appl1
2	56	100.0	117	3	US-08-545-809A-96		Sequence 96, Appl1
3	49	87.5	200	6	5189147-8		Patent No. 5189147
4	49	87.5	561	3	US-09-192-545-2		Sequence 2, Appl1
5	48	85.7	115	1	US-07-942-245-22		Sequence 22, Appl1
6	47	83.9	119	1	US-08-478-039-65		Sequence 65, Appl1
7	47	83.9	119	1	US-08-476-349A-65		Sequence 65, Appl1
8	45	80.4	20	4	US-09-556-605-6		Sequence 6, Appl1
9	45	80.4	119	4	US-08-602-725-27		Sequence 27, Appl1
10	45	80.4	120	2	US-08-478-039-73		Sequence 73, Appl1
11	45	80.4	128	1	US-08-478-039-102		Sequence 102, Appl1
12	45	80.4	128	1	US-08-476-349A-73		Sequence 73, Appl1
13	45	80.4	128	1	US-08-476-349A-102		Sequence 102, Appl1
14	45	80.4	98	3	US-08-881-037-64		Sequence 64, Appl1
15	44	78.6	113	3	US-08-881-037-18		Sequence 18, Appl1
16	44	78.6	117	3	US-08-545-809A-105		Sequence 105, Appl1
17	44	78.6	121	3	US-08-881-037-65		Sequence 65, Appl1
18	44	78.6	121	3	US-08-881-037-65		Sequence 65, Appl1
19	43	76.8	92	3	US-08-783-853A-84		Sequence 84, Appl1
20	43	76.8	92	4	US-09-344-050-84		Sequence 84, Appl1
21	43	76.8	108	4	US-09-893-896-1		Sequence 1, Appl1
22	43	76.8	108	4	US-09-893-896-3		Sequence 3, Appl1
23	43	76.8	112	3	US-08-783-853A-20		Sequence 20, Appl1
24	43	76.8	112	3	US-08-545-809A-113		Sequence 113, Appl1
25	43	76.8	112	4	US-09-344-050-20		Sequence 20, Appl1
26	43	76.8	118	1	US-08-425-336-124		Sequence 124, Appl1
27	43	76.8	118	1	US-08-425-336-126		Sequence 126, Appl1

28	43	76.8	118	1	US-08-488-113B-124	Sequence 124, App
29	43	76.8	118	1	US-08-488-113B-126	Sequence 126, App
30	43	76.8	118	1	US-08-477-484B-124	Sequence 124, App
31	43	76.8	118	1	US-08-477-484B-126	Sequence 126, App
32	43	76.8	118	1	US-08-107-669D-28	Sequence 28, Appl1
33	43	76.8	118	1	US-08-107-669D-29	Sequence 29, Appl1
34	43	76.8	118	1	US-08-107-669D-66	Sequence 66, Appl1
35	43	76.8	118	1	US-08-107-669D-67	Sequence 67, Appl1
36	43	76.8	118	1	US-08-472-788A-28	Sequence 28, Appl1
37	43	76.8	118	1	US-08-472-788A-29	Sequence 29, Appl1
38	43	76.8	118	1	US-08-472-788A-88	Sequence 88, Appl1
39	43	76.8	118	1	US-08-472-788A-89	Sequence 89, Appl1
40	43	76.8	118	2	US-08-477-531B-28	Sequence 28, Appl1
41	43	76.8	118	2	US-08-477-531B-29	Sequence 29, Appl1
42	43	76.8	118	2	US-08-477-531B-66	Sequence 66, Appl1
43	43	76.8	118	2	US-08-477-531B-67	Sequence 67, Appl1
44	43	76.8	118	2	US-08-646-360-124	Sequence 124, App
45	43	76.8	118	2	US-08-646-360-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-08-888-366-2
; Sequence 2, Application US/08889366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-888-366-2
Query Match      100.0%; Score 56; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      26 GYTFTSYDIN 35

RESULT 2
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-96

Query Match      100.0%; Score 56; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      45 GYTFTSYDIN 54

RESULT 3
5189147-8
; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSER, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METEROIDIMERIC T LYMPHOCYTE RECEPTOR
; ANTI-BODY
; NUMBER OF SEQUENCES: 21

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO: 8
; LENGTH: 200
5189147-8

Query Match      87.5%; Score 49; DB 6; Length 200;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      26 GYTFTSYGIN 35

RESULT 4
US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuoka, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2

Query Match      87.5%; Score 49; DB 3; Length 561;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYTFTSYDIN 10
DB      45 GYTFTSYGIN 54

RESULT 5
US-07-942-245-22
; Sequence 22, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States

```

ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-22

Query Match 85.7%; Score 48; DB 1; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.43;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
|||
DB 26 GYTFTSYGVN 35

RESULT 6

US-08-478-039-65
; Sequence 65, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Monkey
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: clone 1-14
US-08-478-039-65

Query Match 83.9%; Score 47; DB 1; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTFTSYDIN 10
|||
DB 26 GYTFTSYVIN 35

RESULT 7

US-08-476-349A-65
; Sequence 65, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Monkey
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT: clone 1-14
 ; US-08-476-349A-55

Query Match 83.9%; Score 47; DB 1; Length 119;
 Best Local Similarity 90.0%; Pred. No. 0.65;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 |||||
 Db 26 GYFTSYIN 35

RESULT 8
 US-09-556-605-6
 ; Sequence 6, Application US/09556605
 ; Patent No. 6417324
 ; GENERAL INFORMATION:
 ; APPLICANT: Salberg, Matti
 ; APPLICANT: Lazdina, Una
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
 ; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
 ; FILE REFERENCE: TRIPEP.020A
 ; CURRENT APPLICATION NUMBER: US/09/556,605
 ; CURRENT FILING DATE: 2000-04-21
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Oligonucleotide
 ; US-09-556-605-6

Query Match 80.4%; Score 45; DB 4; Length 20;
 Best Local Similarity 80.0%; Pred. No. 0.22;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 |||||
 Db 5 GYFTSYDID 14

RESULT 9
 US-09-556-605-1
 ; Sequence 1, Application US/09556605
 ; Patent No. 6417324
 ; GENERAL INFORMATION:
 ; APPLICANT: Salberg, Matti
 ; APPLICANT: Lazdina, Una
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
 ; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
 ; FILE REFERENCE: TRIPEP.020A
 ; CURRENT APPLICATION NUMBER: US/09/556,605
 ; CURRENT FILING DATE: 2000-04-21
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Oligonucleotide
 ; US-09-556-605-1

Query Match 80.4%; Score 45; DB 4; Length 119;

Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 |||||
 Db 25 GYFTSYDID 34

RESULT 10
 US-08-602-725-27
 ; Sequence 27, Application US/08602725
 ; Patent No. 5965710
 ; GENERAL INFORMATION:
 ; APPLICANT: BODMER, WALTER F
 ; APPLICANT: DURBIN, HELGA
 ; APPLICANT: SNARY, DAVID
 ; APPLICANT: STEWART, LORNA MD
 ; APPLICANT: YOUNG, SUSAN
 ; APPLICANT: BATES, PAUL A
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,725
 ; FILING DATE: 02-FEB-1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA: PCT/GB94/01816
 ; FILING DATE: 19-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9317423
 ; FILING DATE: 21-AUG-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36663
 ; REFERENCE/DOCKET NUMBER: 1090-8
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4091
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Human RF-TS3 heavy chain
 ; US-08-602-725-27

Query Match 80.4%; Score 45; DB 2; Length 120;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYFTSYDIN 10
 |||||
 Db 26 GYFTSYAMN 35

```

RESULT 11
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

```

```

Query Match      80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GYFTTSYDIN 10
|:|:|:|:|:|:|
Db      26 GFTFSYDMN 35

```

```

RESULT 12
US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:

```

```

; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-478-039-102

```

```

Query Match      80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GYFTTSYDIN 10
|:|:|:|:|:|:|
Db      26 GFTFSYDMN 35

```

```

RESULT 13
US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Query Match 80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSSYDIN 10
Db 26 GYTFSSYDIN 35

RESULT 14
US-08-476-349A-102
Sequence 102. Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 80.4%; Score 45; DB 1; Length 128;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTFSSYDIN 10
Db 26 GYTFSSYDIN 35

RESULT 15
US-08-881-037-64
Sequence 64. Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037

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; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Koneki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-881-037-64

Query Match      78.6%; Score 44; DB 3; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYFTTSYDIN 10
Db      26 GYFTTSYGIS 35

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Search completed: April 21, 2004, 17:40:03
Job time : 13.029 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 13.6957 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ2
Perfect score: 82
Sequence: 1 inpsngtdyackfq 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	87.8	98	2 S26918	Ig heavy chain V r
2	72	87.8	132	2 S31596	Ig heavy chain V r
3	72	87.8	136	2 S31600	Ig heavy chain V r
4	71	86.6	98	2 S26910	Ig heavy chain V r
5	71	86.6	98	2 S26938	Ig heavy chain V r
6	71	86.6	98	2 S26912	Ig heavy chain V r
7	71	86.6	117	1 HVHJ35	Ig heavy chain pre
8	71	86.6	117	2 S31680	Ig heavy chain V r
9	71	86.6	117	2 S31851	Ig heavy chain V r
10	71	86.6	118	2 S36265	Ig heavy chain V r
11	71	86.6	129	2 S46393	Ig heavy chain V r
12	71	86.6	135	2 S49530	anti-Sm antibody V
13	69	84.1	104	2 S59899	Ig heavy chain V-1
14	68	82.9	123	2 S35548	Ig heavy chain V r
15	65	79.3	171	2 S31623	Ig heavy chain V r
16	63	76.8	110	2 PH1668	Ig heavy chain V r
17	63	76.8	110	2 PH1669	Ig heavy chain V r
18	63	76.8	127	2 S34014	Ig heavy chain V r
19	62	75.6	98	2 S26920	Ig heavy chain V r
20	62	75.6	117	1 HVHJ35	Ig heavy chain pre
21	62	75.6	143	1 EAHJND	Ig heavy chain pre
22	61	74.4	110	2 PH1670	Ig heavy chain V r
23	61	74.4	113	2 S55535	Ig heavy chain V r
24	61	74.4	116	2 S22553	Ig heavy chain V r
25	60	73.2	288	2 S29544	Ig heavy chain VDJ
26	59	72.0	86	2 S29544	Ig heavy chain V r
27	59	72.0	98	2 S26921	Ig heavy chain V r
28	58	70.7	71	2 PH1667	Ig heavy chain V r
29	58	70.7	104	2 PH1665	Ig heavy chain V r

30	58	70.7	114	2 PH1667	Ig heavy chain V r
31	58	70.7	118	2 PH1666	Ig heavy chain V r
32	57	69.5	117	1 MHMS4E	Ig heavy chain V r
33	57	69.5	117	1 MHMSJ5	Ig heavy chain V r
34	57	69.5	118	1 MHMSJ5	Ig heavy chain V r
35	57	69.5	128	2 I37267	Ig heavy chain V r
36	57	69.5	140	2 T01407	Ig heavy chain (my
37	57	69.5	142	2 A32483	Ig heavy chain V r
38	55	67.1	98	2 PH1156	Ig heavy chain V r
39	55	67.1	102	2 S26471	Ig heavy chain V r
40	55	67.1	106	2 PH1005	Ig heavy chain V r
41	55	67.1	117	2 S18553	Ig heavy chain V r
42	54	65.9	96	2 S17230	Ig heavy chain V r
43	54	65.9	96	2 S17618	Ig heavy chain V r
44	54	65.9	96	2 S17620	Ig heavy chain V r
45	54	65.9	96	2 S17614	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26918
Ig heavy chain V region (DP-15) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885, MUID:93021117, PMID:1404388
A:Accession: S26918
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12317; NID:G32857; PIDN:CAA78187.1; PID:G32858
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 72; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 4.5e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYACKFQ 15
Db 51 MAPNSGNTGYACKFQ 65

RESULT 2

S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CU1>
A:Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 72; DB 2; Length 132;
Best Local Similarity 86.7%; Pred. No. 6.2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYACKFQ 15

Db 70 MNPSGNTGYAOKFQ 84
:|||||||

RESULT 3

IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CU>
A:Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 72; DB 2; Length 136;
Best Local Similarity 86.7%; Pred. No. 6.4e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 70 MNPSGNTGYAOKFQ 84

RESULT 4

IG heavy chain V region (DP-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S26910
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26910
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12303; NID:G32847; PIDN:CAA78173.1; PID:G32848
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 51 INPNSGNTGYAOKFQ 65

RESULT 5

IG heavy chain V region (DP-75) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26938
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26938
A>Status: preliminary
A:Molecule type: DNA
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z14071; NID:G32969; PIDN:CAA78451.1; PID:G32970
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 51 INPNSGNTGYAOKFQ 65

RESULT 6

IG heavy chain V region (DP-8) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26912
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26912
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12310; NID:G32979; PIDN:CAA78180.1; PID:G32980
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 98;
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAOKFQ 15
:|||||||

Db 51 INPNSGNTGYAOKFQ 65

RESULT 7

IG heavy chain precursor V region (V35) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C:Accession: S00476; S34013
R:Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuhara, J.
EMBO J. 7, 1047-1051, 1988
A:Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain loc
A:Reference number: S00476; MUID:88296408; PMID:2841108
A:Accession: S00476
A:Molecule type: DNA
A:Residues: 1-117 <MATS>
A:Cross-references: EMBL:X07448; NID:G33104; PIDN:CAB56703.1; PID:G6002173
A:Note: the authors translated the codon AGT for residue 89 as Met
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal J

A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34013
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 20-116 <MAR>

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 1; Length 117;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 70 INPNSGGTNYAQKFQ 84

RESULT 8
 S31680
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S31680
 R;Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
 submitted to the EMBL Data Library, June 1992
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A;Reference number: S31585
 A;Accession: S31680
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-117 <CUI>
 A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
 C;Genetics:
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 117;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 70 INPNSGGTNYAQKFQ 84

RESULT 9
 S18551
 Ig heavy chain V region precursor (VI-2) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
 C;Accession: S18551; S23625
 R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
 EMO J. 10, 3641-3645, 1991
 A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
 A;Reference number: S18551; MUID:92037524; PMID:1935893
 A;Accession: S18551
 A;Molecule type: DNA
 A;Residues: 1-117 <SHI>
 A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Detos, M.; Kozin, F.; Carson, D.A.;
 J. Exp. Med. 175, 831-842, 1992
 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b
 A;Reference number: S23623; MUID:92156804; PMID:1740665
 A;Accession: S23625
 A;Molecule type: DNA
 A;Residues: 1-117 <OLE>
 A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
 C;Genetics:
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 117;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 70 INPNSGGTNYAQKFQ 84

RESULT 10
 S36265
 Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C;Accession: S36265
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.
 A;Reference number: S36256; MUID:93178448; PMID:7679990
 A;Accession: S36265
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-118 <GRI>
 A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 118;
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 51 INPNSGGTNYAQKFQ 65

RESULT 11
 S46393
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S46393
 R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 J. Mol. Biol. 239, 68-78, 1994
 A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
 A;Reference number: S46390; MUID:94254092; PMID:8196048
 A;Accession: S46393
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-129 <FIG>
 A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 129;
 Best Local Similarity 86.7%; Pred. No. 8.9e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 |||||:|||||
 Db 51 INPNSGGTNYAQKFQ 65

RESULT 12
 S49530
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C;Accession: S49530
 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.

A:Reference number: S48797
 A:Accession: S49530
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <MAH>
 A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID:G560840
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 71; DB 2; Length 135;
 Best Local Similarity 86.7%; Pred. No. 9.4e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 DB- 70 INPNSGGTNYAQKFQ 84

RESULT 13

S69899
 Ig heavy chain V region (clone RFT57H), rheumatoid factor - human

C:Species: Homo sapiens (man)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S69899

R:Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J.
 Eur. J. Immunol. 23, 1220-1225, 1993
 A:Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune response
 A:Reference number: S69896; MUID:93272805; PMID:8500520
 A:Accession: S69899

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-104 <RAN>

A:Cross-references: EMBL:Z34993; NID:G509803; PIDN:CAA84376.1; PID:G509804

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 69; DB 2; Length 104;
 Best Local Similarity 86.7%; Pred. No. 0.00016;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 DB- 51 INPNSGGTNYAQKFQ 65

RESULT 14

D33548

Ig heavy chain V-1 region (WIL2) - human

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996

C:Accession: D33548

R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression

A:Reference number: A33548; MUID:89345575; PMID:2503826

A:Accession: D33548

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-123 <KIP>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 68; DB 2; Length 123;
 Best Local Similarity 80.0%; Pred. No. 0.00027;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 DB- 51 INPNSGGTNYAQKFQ 65

RESULT 15

S23623

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R:Ollee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.; (

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23623

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <OLE>

A:Cross-references: EMBL:X59702; NID:G32010; PIDN:CAA42223.1; PID:G32011

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 65; DB 2; Length 171;
 Best Local Similarity 80.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 DB- 70 INPNSGGTGYGQKFQ 84

Search completed: April 21, 2004, 17:38:27

Job time: 13.6957 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 40 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ2

Perfect score: 82
Sequence: 1 inpsngntdyackfq 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	64	78.0	125	4 Q9UL95	Q9ul95 homo sapien
2	63	76.8	119	4 Q9UL94	Q9ul94 homo sapien
3	62	75.6	124	4 Q9UL92	Q9ul92 homo sapien
4	62	75.6	497	4 Q8WY24	Q8wy24 homo sapien
5	59	72.0	614	4 Q96GA6	Q96ga6 homo sapien
6	58	70.7	278	11 Q921K1	Q921k1 mus musculus
7	57	69.5	117	11 Q9QXE9	Q9qxe9 mus musculus
8	57	69.5	117	11 Q9QXF0	Q9qxf0 mus musculus
9	54	65.9	110	11 Q9JL77	Q9jl77 mus musculus
10	52	63.4	159	4 Q96Q50	Q96qa0 homo sapien
11	52	63.4	470	11 Q7RWK1	Q7rwm1 mus musculus
12	51	62.2	137	11 Q924R6	Q924r6 mus musculus
13	51	62.2	139	11 Q924R5	Q924r5 mus musculus
14	51	62.2	140	11 Q924R2	Q924r2 mus musculus
15	51	62.2	141	11 Q924Q4	Q924q4 mus musculus
16	51	62.2	143	11 Q91VA2	Q91va2 mus musculus

17	51	62.2	143	11	Q924Q5	Q924q5 mus musculus
18	51	62.2	143	11	Q924R7	Q924r7 mus musculus
19	51	62.2	143	11	Q924R0	Q924r0 mus musculus
20	51	62.2	144	11	Q924P5	Q924p5 mus musculus
21	51	62.2	145	11	Q924Q6	Q924q6 mus musculus
22	51	62.2	145	11	Q924Q9	Q924q9 mus musculus
23	51	62.2	145	11	Q924R3	Q924r3 mus musculus
24	51	62.2	145	11	Q924Q7	Q924q7 mus musculus
25	51	62.2	145	11	Q924P7	Q924p7 mus musculus
26	51	62.2	145	11	Q924R1	Q924r1 mus musculus
27	51	62.2	145	11	Q924R4	Q924r4 mus musculus
28	51	62.2	146	11	Q924R8	Q924r8 mus musculus
29	51	62.2	146	11	Q924Q3	Q924q3 mus musculus
30	51	62.2	146	11	Q924Q8	Q924q8 mus musculus
31	51	62.2	148	11	Q8K172	Q8k172 mus musculus
32	50	61.0	140	11	Q924P8	Q924p8 mus musculus
33	50	61.0	142	11	Q924Q1	Q924q1 mus musculus
34	49	59.8	119	5	Q9GY22	Q9gy22 schistosoma
35	49	59.8	463	11	Q91LC4	Q91lc4 mus musculus
36	49	59.8	488	11	Q91WR1	Q91wr1 mus musculus
37	49	59.8	500	4	Q9BRV0	Q9brv0 homo sapien
38	48	58.5	468	11	Q99L31	Q99l31 mus musculus
39	48	58.5	488	11	Q8K0F2	Q8k0f2 mus musculus
40	47	57.3	123	11	Q8VIJ1	Q8vij1 mus musculus
41	47	57.3	6077	12	Q91L85	Q91l85 white spot
42	47	57.3	6077	12	Q8VAP1	Q8vap1 white spot
43	47	57.3	6077	12	Q8QFB7	Q8qfb7 white spot
44	44	54.9	118	11	Q921C4	Q921c4 mus musculus
45	45	54.9	143	11	Q924Q0	Q924q0 mus musculus

ALIGNMENTS

RESULT 1
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01810; 2FEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CDS232488EAC CRC64;

Query Match 78.0%; Score 64; DB 4; Length 125;
Best Local Similarity 80.0%; Pred. No. 0.0064;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYACKFQ 15

Db 51 INPNSGGTNYACKVQ 65

```
RESULT 2
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
  (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
FT NON_TER 1
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345FA16E CRC64;

Query Match 76.8%; Score 63; DB 4; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.009;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
  ||||| :|||
Db 51 INPNSGNTDYAQKFQ 65
  ||||| :|||

RESULT 3
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
  (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 124
FT NON_TER 124
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SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 75.6%; Score 62; DB 4; Length 124;
Best Local Similarity 73.3%; Pred. No. 0.014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
  ||||| :|||
Db 51 INPNSGNTDYAQKFQ 65
  ||||| :|||

RESULT 4
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SMC66, a ig-like gene which is
  down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00230; IG_MHC; 1.
DR PROSITE; PS00230; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 75.6%; Score 62; DB 4; Length 497;
Best Local Similarity 66.7%; Pred. No. 0.066;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
  ||||| :|||
Db 70 MNPQNTGTEFAQKFQ 84
  ||||| :|||

RESULT 5
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RT Tissue=B-cell;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AA09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHarac.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_VHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 72.0%; Score 59; DB 4; Length 614;
Best Local Similarity 73.3%; Pred. No. 0.27;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 70 ITPFNGNTYAKRFQ 84

RESULT 6
Q921K1 Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 13, Created)
DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 70.7%; Score 58; DB 11; Length 278;
Best Local Similarity 66.7%; Pred. No. 0.16;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 70 INPNSGNTDYAKRFQ 84

RESULT 7
Q9QXE9 Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR PIR; F33932; F33932.
DR HSP; P01810; 2FSJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR NON TER 117
FT NON TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 69.5%; Score 57; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.088; 3; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGNTSYNQKFK 65

RESULT 8
Q9QXF0 Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR HSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR NON TER 117
FT NON TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 69.5%; Score 57; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.088; 3; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGNTSYNQKFK 65

RESULT 9
Q9JL77 Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mycosin immunoglobulin heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Radenaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR PIR; F33932; F33932.
DR HSP; P01810; 2FSJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

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DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;

Query Match 62.2%; Score 51; DB 11; Length 137;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   :|||||:|:|:
Db 51 IDPNSGGTKYNEKFK 65

RESULT 13
Q924R5 PRELIMINARY; PRT; 139 AA.
AC Q924R5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 139
SQ SEQUENCE 139 AA; 15221 MW; 8491E2F85614736A CRC64;

Query Match 62.2%; Score 51; DB 11; Length 139;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   :|||||:|:|:
Db 51 IDPNSGGTKYNEKFK 65

RESULT 14
Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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```

DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 62.2%; Score 51; DB 11; Length 140;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
   :|||||:|:|:
Db 51 IDPNSGGTKYNEKFK 65

RESULT 15
Q924Q4 PRELIMINARY; PRT; 141 AA.
AC Q924Q4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";

```


RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB067796; BAB63281.1; -.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 141
SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match 62.2%; Score 51; DB 11; Length 141;

Best Local Similarity 60.0%; Pred. No. 1.1;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPNSGNTDYACKFQ 15
Db :|||||:|:
51 IDPNSGGTKYNEKFK 65

Search completed: April 21, 2004, 17:37:14
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 60 seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ2
Perfect score: 82
Sequence: 1 inpsngtdyackfg 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	77	93.9	248	5	ABP45370	Abp45370 Human Bly
2	75	91.5	241	5	ABP45937	Abp45937 Human Bly
3	75	91.5	249	5	ABP45880	Abp45880 Human Bly
4	72	87.8	92	4	AAW20077	Aam20077 Peptide #
5	72	87.8	92	4	AAW33913	Aam33913 Peptide #
6	72	87.8	92	4	ABG55467	Abg55467 Human liv
7	72	87.8	92	5	ABG43604	Abg43604 Human pep
8	72	87.8	98	3	AAV50958	Aay50958 Human FVI
9	72	87.8	98	5	ABG78170	Abg78170 Human Fv
10	72	87.8	98	5	ABG91861	Abg91861 Human ant
11	72	87.8	98	6	ABO27070	Abc27070 Human ger
12	72	87.8	117	2	AAW66302	Aar66302 Human imm
13	72	87.8	121	4	AAU02576	Aau02576 Anti-adip
14	72	87.8	122	6	ABR55829	Abp55829 Heavy cha
15	72	87.8	149	6	ABO04846	Abc04846 Human epi
16	72	87.8	199	2	AAV34302	Aay34302 IGM anti b
17	72	87.8	203	2	AAV34301	Aay34301 IGM anti b
18	72	87.8	241	5	ABP46020	Abp46020 Human Bly
19	72	87.8	247	5	ABP44916	Abp44916 Human Bly
20	72	87.8	247	5	ABP44937	Abp44937 Human Bly
21	72	87.8	249	5	ABP44908	Abp44908 Human Bly
22	71	86.6	17	2	AAW95253	Aaw95253 Anti-prog
23	71	86.6	17	5	AAE28548	Aae28548 scFv anti
24	71	86.6	17	5	AAE28547	Aae28547 scFv anti
25	71	86.6	96	5	ABG78159	Abg78159 Human Fv

26	71	86.6	98	5	ABG78160	Abg78160 Human Fv
27	71	86.6	98	5	ABG78158	Abg78158 Human Fv
28	71	86.6	98	5	ABG78161	Abg78161 Human Fv
29	71	86.6	98	5	ABG78156	Abg78156 Human Fv
30	71	86.6	98	5	ABG91849	Abg91849 Human ant
31	71	86.6	98	5	ABG91851	Abg91851 Human ant
32	71	86.6	98	5	ABG91847	Abg91847 Human ant
33	71	86.6	98	5	ABG91852	Abg91852 Human ant
34	71	86.6	98	5	ABG91850	Abg91850 Human ant
35	71	86.6	98	6	ABJ18688	Abj18688 Antibody
36	71	86.6	98	6	ABO27068	Abc27068 Human ger
37	71	86.6	111	5	ABO07180	Abc07180 CS2iE12 h
38	71	86.6	116	5	ABBS7555	ABBS7555 HLA-DR-sp
39	71	86.6	117	2	AAW66296	Aar66296 Human imm
40	71	86.6	118	6	ADA89115	Ada89115 MS-Pro-2-
41	71	86.6	120	2	AAW27551	Aaw27551 Human Ab
42	71	86.6	120	6	ABJ18719	Abj18719 Antibody
43	71	86.6	120	6	ABJ18673	Abj18673 Antibody
44	71	86.6	123	2	AAW79228	Aaw79228 Heavy cha
45	71	86.6	126	6	ADA89123	Ada89123 MS-Pro-54

ALIGNMENTS

RESULT 1
ABP45370
ID ABP45370 standard; protein; 248 AA.

AC ABP45370;
XX
XX
XX 19-AUG-2002 (first entry)
XX
XX Human BlyS binding scFv SEQ ID 1381.

BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunopressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUNA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2051-2052; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to

XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

XX tumour necrosis factor (TNF) super family and induces B cell

XX proliferation and differentiation. The antibodies of the invention have

XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;
Query Match 93.9%; Score 77; DB 5; Length 248;
Best Local Similarity 93.3%; Pred. No. 6.7e-05; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 0;
QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGNTDYAQKFQ 65
RESULT 2
ABP45937
ID ABP45937 standard; protein; 241 AA.
XX
AC ABP45937;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1948.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
FN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2725-2726; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 241 AA;
Query Match 91.5%; Score 75; DB 5; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGNTGYAQKFQ 65
RESULT 3
ABP45980
ID ABP45980 standard; protein; 249 AA.
XX
AC ABP45980;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1891.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
FN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2658-2659; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of BLYS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLYS. They may also be
 CC administered to treat diseases associated with aberrant BLYS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 XX SQ Sequence 249 AA;

Query Match 91.5%; Score 75; DB 5; Length 249;
 Best Local Similarity 93.3%; Pred. NO. 0.00015;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 :|||||
 Db 51 INPNSGNTDYAQKFQ 65

RESULT 4
 AAM20077
 ID AAM20077 standard; protein; 92 AA.

AC AAM20077;

XX 12-OCT-2001 (first entry)

DE Peptide #6511 encoded by probe for measuring cervical gene expression.
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

OS Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 24903; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see A110068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 92 AA;

Query Match 87.8%; Score 72; DB 4; Length 92;
 Best Local Similarity 86.7%; Pred. NO. 0.00016;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 :|||||
 Db 42 MNPNSGNTGYAQKFQ 56

RESULT 5

AAM33913

ID AAM33913 standard; protein; 92 AA.

XX AAM33913;

XX 17-OCT-2001 (first entry)

DE Peptide #7950 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488997/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 34182; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs:
 CC see A113135-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders

XX SQ Sequence 92 AA;

Query Match 87.8%; Score 72; DB 4; Length 92;
 Best Local Similarity 86.7%; Pred. NO. 0.00016;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
 :|||||
 Db 42 MNPNSGNTGYAQKFQ 56

RESULT 6

ABG55467

ID ABG55467 standard; peptide; 92 AA.

XX

AC AEG55467;
 XX 25-FEB-2003 (first entry)
 DT Human liver peptide, SEQ ID No 34115.
 XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 XX hypercholesterolaemia; coronary heart disease.
 KW Homo sapiens.
 OS WO200157273-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000664.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human adult liver.
 XX Claim 27; SEQ ID NO 34115; 658pp; English.
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 XX measuring human gene expression in a sample derived from human adult
 XX liver, comprising one of 13109 defined nucleotide sequences given in the
 XX specification (or complements/ fragments). The probe hybridises at high
 XX stringency to a nucleic acid molecule expressed in the human adult liver.
 XX (I) may be used for predicting, measuring and displaying gene expression
 XX in samples derived from human adult liver. The genes identified may be
 XX involved in genetic liver diseases such as cirrhosis.
 XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 XX associated with coronary heart disease. ABG47348-ABG5930 represent human
 XX liver single exon encoded peptides of the invention. Note: The sequence
 XX information for this patent does not appear in the printed specification
 XX but was obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 92 AA;
 SQ
 Query Match 87.8%; Score 72; DB 4; Length 92;
 Best Local Similarity 86.7%; Pred. No. 0.00016;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPNSGNTDYAQKFQ 15
 Db 42 MNPNSGNTGYAQKFQ 56
 .|||||
 .|||||
 RESULT 7
 ABG43604
 ID ABG43604 standard; peptide; 92 AA.
 XX AC ABG43604;
 XX 19-AUG-2002 (first entry)
 DT Human peptide encoded by genome-derived single exon probe SEQ ID 33269.
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW

chronic obstructive pulmonary disease; interstitial lung disease;
 familial idiopathic pulmonary fibrosis; neurofibromatosis;
 tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 primary ciliary dyskinesia; pulmonary hypertension;
 hyaline membrane disease.
 XX Homo sapiens.
 OS WO200186003-A2.
 XX 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 XX Claim 27; SEQ ID NO 33269; 634pp; English.
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human lung comprising single exon nucleic acid probes having one of
 XX 12614 nucleic acid sequences mentioned in the specification, or their
 XX complements or the 12614 open reading frames derived from the 12614
 XX probes. Also included are a microarray comprising the novel set of probes
 XX; the novel set of probes which hybridise at high stringency to a nucleic
 XX acid expressed in the human lung; measuring gene expression in a sample
 XX derived from human lung, comprising (a) contacting the array with a
 XX collection of detectably labeled nucleic acids derived from human lung
 XX mRNA, and (b) measuring the label detectably bound to each probe of the
 XX array; identifying exons in a eukaryotic genome, comprising (a)
 XX algorithmically predicting at least one exon from genomic sequences of
 XX the eukaryote; and (b) detecting specific hybridisation of detectably
 XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 XX having a fragment identical to the predicted exon, the probe is included
 XX in the above mentioned microarray; assigning exons to a single gene,
 XX comprising (a) identifying exons from genomic sequence by the method
 XX above and (b) measuring the expression of each of the exons in several
 XX tissues and/or cell types using hybridisation to a single exon
 XX microarrays having a probe with the exon, where a common pattern of
 XX expression of the exons in the tissues and/or cell types comprising one
 XX of the exons should be assigned to a single gene; a peptide comprising one
 XX of 12011 sequences, mentioned in the specification, or encoded by the
 XX probes/open reading frames (ORF). The probes are used for gene expression
 XX analysis, and for identifying exons in a gene, particularly using human
 XX lung derived mRNA and for the study of lung diseases such as asthma, lung
 XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 XX present sequence is a peptide/protein encoded by a single exon probe of
 XX the invention. Note: The sequence data for this patent did not form part
 XX of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 92 AA;
 XX Query Match 87.8%; Score 72; DB 5; Length 92;
 XX Best Local Similarity 86.7%; Pred. No. 0.00016;
 XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPNSGNTDYAQKFQ 15
 :|||||
 DB 42 MNPNSGNTGYAQKFQ 56
 :|||||
 RESULT 8
 AAY50558
 ID AAY50558 standard; protein; 98 AA.
 XX
 AC AAY50558;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
 XX
 KW Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A;
 KW scFv; A3-C1.
 XX
 OS Homo sapiens.
 XX
 PN WO9955680-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-NL000285.
 XX
 PR 08-MAY-1998; 98EP-00201543.
 XX
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
 XX
 PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
 XX WPI; 2000-053102/04.
 XX
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for treatment
 PT of hemophilia A patients with these antibodies.
 XX
 PS Example 8; Fig 9A; 61pp; English.
 CC This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specificity which has
 CC hemostatic activity. (I) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them are
 CC useful in compositions for neutralizing factor VIII inhibiting antibodies
 CC in hemophilia A patients. This sequence represents the human factor VIII
 CC antibody A3-C1 specific scFv protein DP-15 which is used in the method of
 CC the invention
 XX
 SQ Sequence 98 AA;
 XX Query Match 87.8%; Score 72; DB 3; Length 98;
 XX Best Local Similarity 86.7%; Pred. No. 0.00017;
 XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPNSGNTDYAQKFQ 15
 :|||||
 DB 51 MNPNSGNTGYAQKFQ 65
 :|||||
 RESULT 9
 ABG78170
 ID ABG78170 standard; protein; 98 AA.

XX ABG78170;
 AC
 XX 15-NOV-2002 (first entry)
 DT
 XX Human Fv molecule hypervariable region related peptide #45.
 DE
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX WPI; 2002-619166/66.
 DR
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 PS Claim 13; Page 168-169; 232pp; English.
 XX
 CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 SQ Sequence 98 AA;
 XX Query Match 87.8%; Score 72; DB 5; Length 98;
 XX Best Local Similarity 86.7%; Pred. No. 0.00017;
 XX Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPNSGNTDYAQKFQ 15
 :|||||
 DB 51 MNPNSGNTGYAQKFQ 65
 :|||||
 RESULT 10
 ABG91861
 ID ABG91861 standard; protein; 98 AA.
 XX
 AC ABG91861;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #45.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 FN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 XX 31-DEC-2001; 2001WO-US049442.
 XX
 XX 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon B, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 DR
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 XX Disclosure; Page 246; Opp; English.
 PS
 XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 XX Sequence 98 AA;
 SQ
 Query Match 87.8%; Score 72; DB 5; Length 98;
 Best Local Similarity 86.7%; Pred. No. 0.00017;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPNSGNTDYAQKFQ 15
 Db 51 MNPNSGNTGYAQKFQ 65
 :|||||
 RESULT 11
 ABO27070
 ID ABO27070 standard; protein; 98 AA.
 XX
 AC ABO27070;
 XX
 DT 10-SEP-2003 (first entry)
 XX
 DE Human germline heavy chain variable region gene segment #3.
 XX

KW Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.
 XX
 OS Homo sapiens.
 XX
 FN US2003039649-A1.
 XX
 PD 27-FEB-2003.
 XX
 XX 12-JUL-2002; 2002US-00194975.
 PF
 XX 12-JUL-2001; 2001US-0305111P.
 PR
 XX (FOOT/) FOOTE J.
 PA
 XX Foote J;
 PI
 XX WPI; 2003-492151/46.
 DR
 XX Making humanized antibody for converting antibody, by making chimeric
 PT antibodies containing complementarity determining region from non-human
 PT antibody and appropriate framework sequences of human antibodies.
 XX
 XX Example 1; Fig 1; 3ipp; English.
 PS
 XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies
 XX
 XX Sequence 98 AA;
 SQ
 Query Match 87.8%; Score 72; DB 6; Length 98;
 Best Local Similarity 86.7%; Pred. No. 0.00017;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPNSGNTDYAQKFQ 15
 Db 51 MNPNSGNTGYAQKFQ 65
 :|||||
 RESULT 12
 AAR66302
 ID AAR66302 standard; protein; 117 AA.
 XX
 AC AAR66302;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-AUG-1995 (first entry)
 XX
 DE Human immunoglobulin variable heavy chain #8.
 XX
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.Coli; mammalian.
 XX

```
OS Homo sapiens.
XX WO9426895-A1.
XX 24-NOV-1994.
XX 10-MAY-1993; 93WO-JP000603.
XX 10-MAY-1993; 93WO-JP000603.
XX (NIBS ) JAPAN TOBACCO INC.
XX
XX Honjo T, Matsuda F;
XX WPI; 1995-006791/01.
XX N-PSDB; AAQ78946.
XX
XX DNA fragment comprising human immunoglobulin Vh genes - for the
XX production of human immunoglobulin in mammalian hosts.
XX
XX Claim 17; Page 41-42; 130pp; Japanese.
XX
XX Protein sequences (AAR6295-51) are novel human immunoglobulin heavy
XX chain sequences encoded by novel isolated genes. The genes (AAQ78939-
XX 79002) were isolated and cloned from a series of cosmid constructs: Y202;
XX Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using
XX primers AAQ78917-38. The genes are subdivided into 5 families of Vh
XX genes. The fragments cover a region of 800 kb. The DNA fragments were
XX isolated from high molecular weight DNA from human placenta. The DNA was
XX partially digested with TaqI restriction enzyme. The fragments were
XX separated by gel electrophoresis and 35-45 kb fractions were collected.
XX The fragments were ligated with ClaI-digested cosmid vector pUBS1. The
XX ligation products were in vitro packed and infected into E.coli 490A. The
XX fragments were then subcloned by colony hybridisation. The Vh genes and
XX the DNA fragments encoding them are useful in producing human
XX immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 117 AA;
QY 1 INPNSGNTDYAQKFQ 15
DB 70 MNPNSGNTGYAQKFQ 84

Query Match 87.8%; Score 72; DB 2; Length 117;
Best Local Similarity 86.7%; Pred. No. 0.00021;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 70 MNPNSGNTGYAQKFQ 84

RESULT 13
AAU02576
ID AAU02576 standard; protein; 121 AA.
XX
XX AAU02576;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody heavy chain, FAT 64.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX

XX PI Edwards BM, Main SH, Vaughan TJ;
XX WPI; 2001-282031/29.
XX N-ESDB; AAS03476.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX Claim 1; Page 140; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX Sequence 121 AA;
QY 1 INPNSGNTDYAQKFQ 15
DB 51 MNPNSGNTGYAQKFQ 65

Query Match 87.8%; Score 72; DB 4; Length 121;
Best Local Similarity 86.7%; Pred. No. 0.00021;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 MNPNSGNTGYAQKFQ 65

RESULT 14
ABR55829
ID ABR55829 standard; protein; 122 AA.
XX
XX ABR55829;
XX
XX 02-SEP-2003 (first entry)
XX
XX Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC.
XX
XX Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
XX Gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
XX angiogenesis; antibody.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 26..36
XX /note= "complementarity determining region (CDR) 1"
XX Region 50..66
XX /note= "complementarity determining region (CDR) 2"
XX Region 96..112
XX /note= "complementarity determining region (CDR) 3"
XX
XX WO2003030833-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032613.
XX
XX 11-OCT-2001; 2001US-0328604P.
XX
XX 10-OCT-2002; 2002US-00269805.
XX
```


DR	N-PSDB; ACD10930.
XX	
PT	Fully human monoclonal antibodies that bind to epidermal growth factor
XX	receptors, useful in cancer therapy.
PP	
PS	Example 3; Fig 59; 100pp; English.
XX	
CC	The invention relates to an antibody that binds to an epidermal growth
CC	factor receptor (EGF-r) and exhibits inhibition of tyrosine
CC	phosphorylation of EGF-2, the degradation of EGF-r, the EGF induced
CC	degradation of EGF-r, vascular endothelial cell growth factor (VEGF)
CC	production by tumour cells (by greater than 50%) and endothelial cells
CC	(by greater than 40%) and also protects threonine phosphorylation of EGF-
CC	r and a 63KD protein. The antibody is internalised with EGF-r. The
CC	antibody may be used for treating tumours such as lung tumours and colon
CC	tumours and for treating inflammation and autoimmune diseases. Sequences
CC	ABO04824-ABO04859 represent human EGF-r receptor antibodies of the
CC	invention
XX	
SQ	Sequence 149 AA;
	Query Match 87.8%; Score 72; DB 6; Length 149;
	Best Local Similarity 86.7%; Pred. No. 0.00027;
	Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY	1 INPNSGNTDYAQKFQ 15 :
Db	39 MNPNSGNTGYAQKFQ 53 :

Sequence 53, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 5, Appl
Sequence 127, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 28, Appl
Sequence 42, Appl
Sequence 19, Appl

60 73.2 128 5 PCT-US95-08743-53
60 73.2 128 5 PCT-US95-08743-55
60 73.2 128 5 PCT-US95-08743-56
60 73.2 137 3 US-08-513-968-38
59 72.0 110 4 US-09-899-896-5
59 72.0 117 3 US-08-545-809A-127
59 72.0 128 1 US-08-276-852-58
59 72.0 128 1 US-08-899-575-58
59 72.0 128 1 PCT-US95-08743-58
59 72.0 137 3 US-08-444-644-17
58 70.7 137 4 US-08-232-246A-17
58 70.7 233 3 US-08-444-644-33
58 70.7 233 4 US-08-232-246A-33
58 70.7 235 3 US-08-444-644-19
58 70.7 235 3 US-08-444-644-28
58 70.7 235 3 US-08-444-644-42
58 70.7 235 4 US-08-232-246A-19

ALIGNMENTS

RESULT 1
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-22

Query Match 93.9%; Score 77; DB 4; Length 117;
Best Local Similarity 93.3%; Pred. No. 9.2e-06;
Matches 14; Conservative 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model
Run on: April 21, 2004, 17:28:28 ; Search time 18.0435 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ2
Perfect score: 82
Sequence: 1 inpnegndyagkfq 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	93.9	117	4	US-09-025-769B-22
2	72	87.8	117	3	US-08-545-809A-96
3	71	86.6	117	4	US-09-424-712-21
4	71	86.6	117	3	US-08-545-809A-90
5	71	86.6	120	4	US-09-025-769B-36
6	71	86.6	120	4	US-09-025-769B-59
7	71	86.6	123	1	US-08-477-877B-94
8	71	86.6	123	2	US-08-472-881A-94
9	71	86.6	123	2	US-08-477-989B-94
10	67	81.7	119	1	US-08-478-039-65
11	67	81.7	119	1	US-08-476-349A-65
12	62	75.6	97	2	US-08-290-592E-16
13	62	75.6	97	5	PCT-US95-10053-13
14	62	75.6	97	5	PCT-US96-09448-16
15	62	75.6	117	3	US-08-545-809A-128
16	60	73.2	118	1	US-08-491-845-6
17	60	73.2	118	1	US-08-491-845-14
18	60	73.2	119	4	US-09-438-954-4
19	60	73.2	128	1	US-08-276-852-53
20	60	73.2	128	1	US-08-276-852-55
21	60	73.2	128	1	US-08-276-852-56
22	60	73.2	128	1	US-08-899-575-53
23	60	73.2	128	1	US-08-899-575-55
24	60	73.2	128	1	US-08-899-575-56
25	60	73.2	128	1	US-08-899-575-53
26	60	73.2	128	1	US-08-899-575-55
27	60	73.2	128	1	US-08-899-575-56

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QY      1 INPNSGNTDYAQKFQ 15
DB      51 INPNSGNTNYAQKFQ 65

RESULT 2
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-96

Query Match      87.8%; Score 72; DB 3; Length 117;
Best Local Similarity 86.7%; Pred. No. 6.4e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
DB      70 MNPNSGNTGYAQKFQ 84

RESULT 3
US-09-424-712-21
; Sequence 21, Application US/09424712
; Patent No. 6620587
; GENERAL INFORMATION:
; APPLICANT: TAUSIG, Michael John
; APPLICANT: HE, Mingyue
; TITLE OF INVENTION: RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AN
; TITLE OF INVENTION: EVOLUTION OF PROTEINS
; FILE REFERENCE: 37945-0017
; CURRENT APPLICATION NUMBER: US/09/424,712
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/GB98/01564
; PRIOR FILING DATE: 1998-05-28
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; PRIOR APPLICATION NUMBER: GB 9804195.7
; PRIOR FILING DATE: 1998-02-28
; PRIOR APPLICATION NUMBER: GB 9724850.4
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: GB 9710829.4
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-712-21

Query Match      86.6%; Score 71; DB 4; Length 117;
Best Local Similarity 86.7%; Pred. No. 1.2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
DB      2 INPNSGNTNYAQKFQ 16

RESULT 4
US-08-545-809A-90
; Sequence 90, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-90

Query Match      86.6%; Score 71; DB 3; Length 117;
Best Local Similarity 86.7%; Pred. No. 9.5e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
DB      1 INPNSGNTDYAQKFQ 15
```

Db 70 INPNSGGTNYAQKFQ 84

RESULT 5

US-09-025-769B-36
; Sequence 36, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: US/09/025,769B
; PRIOR APPLICATION DATA:
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-36

Query Match 86.6%; Score 71; DB 4; Length 120;
Best Local Similarity 86.7%; Pred. No. 9.8e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGGTNYAQKFQ 65

RESULT 6

US-09-025-769B-59
; Sequence 59, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-59

Query Match 86.6%; Score 71; DB 4; Length 120;
Best Local Similarity 86.7%; Pred. No. 9.8e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 51 INPNSGGTNYAQKFQ 65

RESULT 7

US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008

```

; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-477-877B-94

Query Match      86.6%; Score 71; DB 1; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
        |||||..|:|||||
Db      51 INPNSGGTNYAQKFQ 65

RESULT 8
US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable
; TYPE: amino acid
; STRANDEDNESS:
; US-08-477-877B-94

Query Match      86.6%; Score 71; DB 1; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
        |||||..|:|||||
Db      51 INPNSGGTNYAQKFQ 65

RESULT 9
US-08-477-989B-94
; Sequence 94, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable
; TYPE: amino acid
; STRANDEDNESS:
; US-08-477-989B-94
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; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-472-281A-94

Query Match      86.6%; Score 71; DB 2; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 INPNSGNTDYAQKFQ 15
        |||||..|:|||||
Db      51 INPNSGGTNYAQKFQ 65

RESULT 9
US-08-477-989B-94
; Sequence 94, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable
; TYPE: amino acid
; STRANDEDNESS:
; US-08-477-989B-94
```

Query Match 86.6%; Score 71; DB 2; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
|||||:|||||

DB 51 INPNSGGTYAQKFQ 65
|||||:|||||

RESULT 10
US-08-478-039-65
; Sequence 65, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: clone 1-14
US-08-478-039-65

Query Match 81.7%; Score 67; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.00046;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
|||||:|||||

DB 51 INPNSGGTYAQKFQ 65
|||||:|||||

RESULT 12
US-08-290-592B-16

Query Match 81.7%; Score 67; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.00046;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
|||||:|||||

DB 51 INPNSGGTYAQKFQ 65
|||||:|||||

RESULT 12
US-08-290-592B-16

Query Match 81.7%; Score 67; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.00046;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
|||||:|||||

DB 51 INPNSGGTYAQKFQ 65
|||||:|||||

RESULT 12
US-08-290-592B-16

Sequence 16, Application US/08290592E
Patent No. 5824307
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
ADDRESSEE: OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,592E
FILING DATE: August 15, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-290-592E-15

Query Match 75.6%; Score 62; DB 2; Length 97;
Best Local Similarity 73.3%; Pred. No. 0.0026;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 51 INPSGGSTSYAQKFQ 65

RESULT 13
PCT-US95-10053-13
Sequence 13, Application PC/TUS9510053
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytica
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10053

FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 469201-274
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-10053-13

Query Match 75.6%; Score 62; DB 5; Length 97;
Best Local Similarity 73.3%; Pred. No. 0.0026;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 INPNSGNTDYAQKFQ 15
Db 51 INPSGGSTSYAQKFQ 65

RESULT 14
PCT-US96-09448-16
Sequence 16, Application PC/TUS9609448
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytica
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09448
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACID

STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US96-09448-16

Query Match 75.6%; Score 62; DB 5; Length 97;
Best Local Similarity 73.3%; Pred. No. 0.0026; 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKRFQ 15
Db 51 INPSSGGSYSYAKRFQ 65

RESULT 15

US-08-545-809A-128
Sequence 128, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-128

Query Match 75.6%; Score 62; DB 3; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.0031; 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKRFQ 15
Db 70 INPSSGGSYSYAKRFQ 84

Search completed: April 21, 2004, 17:40:03
Job time : 18.0435 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 45,2174 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ2

Perfect score: 82

Sequence: 1 inpsngntdyakfq 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	125	14	US-10-041-860-48
2	82	100.0	125	14	US-10-041-860-200
3	82	100.0	125	14	US-10-041-860-237
4	82	100.0	125	14	US-10-041-860-372
5	79	96.3	98	14	US-10-041-860-373
6	77	93.9	248	10	US-09-880-748-1381
7	77	93.9	248	12	US-10-293-418-1381
8	75	91.5	98	14	US-10-041-860-374
9	75	91.5	241	10	US-09-880-748-1948
10	75	91.5	241	12	US-10-293-418-1948
11	75	91.5	249	10	US-09-880-748-1891
12	75	91.5	249	12	US-10-293-418-1891
13	72	87.8	17	14	US-10-148-844-40
14	72	87.8	92	9	US-09-864-761-47202
15	72	87.8	96	14	US-10-194-975-3

16	72	87.8	98	12	US-10-029-926B-45	Sequence 45, Appl
17	72	87.8	98	14	US-10-041-860-289	Sequence 289, App
18	72	87.8	98	14	US-10-041-860-290	Sequence 290, App
19	72	87.8	98	14	US-10-041-860-295	Sequence 295, App
20	72	87.8	98	14	US-10-041-860-296	Sequence 296, App
21	72	87.8	98	14	US-10-041-860-342	Sequence 342, App
22	72	87.8	98	14	US-10-041-860-344	Sequence 344, App
23	72	87.8	98	14	US-10-041-860-348	Sequence 348, App
24	72	87.8	98	14	US-10-041-860-361	Sequence 361, App
25	72	87.8	98	15	US-10-032-037B-45	Sequence 45, Appl
26	72	87.8	98	15	US-10-029-988B-45	Sequence 45, Appl
27	72	87.8	98	15	US-10-032-423A-45	Sequence 45, Appl
28	72	87.8	99	14	US-10-041-860-1	Sequence 1, Appli
29	72	87.8	122	14	US-10-269-805-61	Sequence 61, Appl
30	72	87.8	125	14	US-10-041-860-38	Sequence 38, Appl
31	72	87.8	125	14	US-10-041-860-203	Sequence 203, App
32	72	87.8	125	14	US-10-041-860-238	Sequence 238, App
33	72	87.8	125	14	US-10-041-860-240	Sequence 240, App
34	72	87.8	125	14	US-10-041-860-343	Sequence 343, App
35	72	87.8	126	14	US-10-041-860-19	Sequence 19, Appl
36	72	87.8	126	14	US-10-041-860-21	Sequence 21, Appl
37	72	87.8	126	14	US-10-041-860-37	Sequence 37, Appl
38	72	87.8	126	14	US-10-041-860-199	Sequence 199, App
39	72	87.8	126	14	US-10-041-860-201	Sequence 201, App
40	72	87.8	126	14	US-10-041-860-202	Sequence 202, App
41	72	87.8	126	14	US-10-041-860-236	Sequence 236, App
42	72	87.8	126	14	US-10-041-860-239	Sequence 239, App
43	72	87.8	126	14	US-10-041-860-288	Sequence 288, App
44	72	87.8	126	14	US-10-041-860-294	Sequence 294, App
45	72	87.8	149	9	US-09-187-693-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1

US-10-041-860-48
; Sequence 48, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-48

Query Match 100.0%; Score 82; DB 14; Length 125;
Best local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAKQFQ 15

Db 51 INPNSGNTDYAKQFQ 65

RESULT 2

US-10-041-860-200
; Sequence 200, Application US/10041860

```

; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-200

```

```

Query Match      100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 INPNSGNTDYAQKFQ 15
|||
Db 51 INPNSGNTDYAQKFQ 65
|||

```

```

RESULT 3
US-10-041-860-237
; Sequence 237, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-237

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```

Query Match      100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 INPNSGNTDYAQKFQ 15
|||
Db 51 INPNSGNTDYAQKFQ 65
|||

```

```

RESULT 4
US-10-041-860-372
; Sequence 372, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.

```

```

; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372

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Query Match      100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 INPNSGNTDYAQKFQ 15
|||
Db 51 INPNSGNTDYAQKFQ 65
|||

```

```

RESULT 5
US-10-041-860-373
; Sequence 373, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-373

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```

Query Match      96.3%; Score 79; DB 14; Length 98;
Best Local Similarity 93.3%; Pred. No. 8.4e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 INPNSGNTDYAQKFQ 15
:|||||
Db 51 MNPNSGNTDYAQKFQ 65
:|||||

```

```

RESULT 6
US-09-880-748-1381
; Sequence 1381, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748

```

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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1381
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1381

Query Match          93.9%; Score 77; DB 10; Length 248;
Best Local Similarity 93.3%; Pred. No. 5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTNYAQKFQ 65

RESULT 7
US-10-293-418-1381
; Sequence 1381, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1381
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1381

Query Match          93.9%; Score 77; DB 12; Length 248;
Best Local Similarity 93.3%; Pred. No. 5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTNYAQKFQ 65

RESULT 8
US-10-041-860-374
; Sequence 374, Application US/10041860
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; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX-051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 59, 73, 97
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 59, 73, 97
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-374

Query Match          91.5%; Score 75; DB 14; Length 98;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
DB 51 INPNSGNTXYAQKFQ 65

RESULT 9
US-09-880-748-1948
; Sequence 1948, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1948
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1948

Query Match          91.5%; Score 75; DB 10; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
```

```
Db      51  INPNSGNTGYAQRKQ 65
|||||
Query Match      91.5%; Score 75; DB 12; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
US-10-293-418-1948
; Sequence 1948, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1948
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1948

Query Match      91.5%; Score 75; DB 12; Length 241;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  INPNSGNTGYAQRKQ 15
|||||
Db      51  INPNSGNTGYAQRKQ 65

Query Match      91.5%; Score 75; DB 12; Length 249;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
US-09-880-748-1891
; Sequence 1891, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1891
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1891

Qy      1  INPNSGNTGYAQRKQ 15
|||||
Db      51  INPNSGNTGYAQRKQ 65

Query Match      91.5%; Score 75; DB 12; Length 249;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
US-10-293-418-1891
; Sequence 1891, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1891
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1891

Qy      1  INPNSGNTGYAQRKQ 15
|||||
Db      51  INPNSGNTGYAQRKQ 65

Query Match      91.5%; Score 75; DB 12; Length 249;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
US-10-148-844-40
; Sequence 40, Application US/10148844
; Publication No. US20030096403A1
; GENERAL INFORMATION:
; APPLICANT: Hye-Jeong Hong
; APPLICANT: Keun-Soo Kim
; TITLE OF INVENTION: A HUMANIZED ANTIBODY TO SURFACE ANTIGEN S OF HEPATITIS B
; FILE REFERENCE: 118.15-US-WO
; CURRENT APPLICATION NUMBER: US/10/148,844
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: KR 2000-57891
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: KR 2001-60966
; PRIOR FILING DATE: 2001-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-148-844-40

Query Match      87.8%; Score 72; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPNSGNTDYAQKFQ 15
Db 2 MNPNSGNTGYAQKFQ 16

RESULT 14
US-09-864-761-47202
; Sequence 47202, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47202
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
```

```
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUATE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUATE 8.00e-48
US-09-864-761-47202
```

```
Query Match      87.8%; Score 72; DB 9; Length 92;
Best Local Similarity 86.7%; Pred. No. 0.00012;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 INPNSGNTDYAQKFQ 15
Db 42 MNPNSGNTGYAQKFQ 56
```

```
RESULT 15
US-10-194-975-3
; Sequence 3, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-3
```

```
Query Match      87.8%; Score 72; DB 14; Length 96;
Best Local Similarity 86.7%; Pred. No. 0.00013;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 INPNSGNTDYAQKFQ 15
Db 49 MNPNSGNTGYAQKFQ 63
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Search completed: April 21, 2004, 18:02:05
Job time : 45.2174 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 64 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ3
Perfect score: 97
Sequence: 1 gfgysynydygmdv 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62.5	64.4	143	6	Aae37203 Human AB-
2	59	60.8	146	5	Aam51172 Human rec
3	57	58.8	112	6	Abp45174 Human DIT
4	56.5	58.2	21	5	Abp46758 Human BLY
5	56.5	58.2	257	5	Abp45542 Human BLY
6	56	57.7	124	5	Abg77138 Anti-IGF-
7	56	57.7	170	4	Aam79672 Human pro
8	56	57.7	384	4	Aam24101 Human EST
9	56	57.7	470	5	Abg77157 Amino aci
10	56	57.7	590	4	Aam78688 Human pro
11	55	56.7	44	5	Abg31313 Human hea
12	55	56.7	128	6	Ada89202 Human ant
13	55	56.7	145	6	Abp57367 Anti-TRAI
14	54	55.7	157	6	Abc004856 Human epi
15	53.5	55.2	18	5	Aau70375 Mouse hea
16	53	54.6	19	5	Abp46976 Human BLY
17	53	54.6	125	5	Abg77142 Anti-IGF-
18	53	54.6	146	5	Aam51170 Human rec
19	53	54.6	146	5	Aam51171 Human rec
20	53	54.6	146	5	Aam51168 Human rec
21	53	54.6	254	5	Abp45614 Human BLY
22	52.5	54.1	24	5	Abp46915 Germ-line
23	52.5	54.1	24	5	Abp46915 Human BLY
24	52.5	54.1	145	6	Aae37205 Human AB-
25	52.5	54.1	260	5	Abp45447 Human BLY

26	52	53.6	17	5	ABP46825	Abp46825 Human BLY
27	52	53.6	19	5	ABP46724	Abp46724 Human BLY
28	52	53.6	24	2	AAW34640	AAW34640 Human occ
29	52	53.6	146	5	AAW51169	AAW51169 Human rec
30	52	53.6	252	5	ABP45404	ABP45404 Human BLY
31	52	53.6	254	5	ABP45248	ABP45248 Human BLY
32	52	53.6	255	5	ABP45273	ABP45273 Human BLY
33	52	53.6	255	5	ABP45260	ABP45260 Human BLY
34	52	53.6	257	5	ABP45272	ABP45272 Human BLY
35	52	53.6	522	2	AAW36052	AAW36052 Human occ
36	52	53.6	522	2	AAW34638	AAW34638 Human occ
37	52	53.6	522	3	ABJ35731	ABJ35731 Human occ
38	52	53.6	522	6	ABJ37076	ABJ37076 Human bre
39	52	53.6	522	7	ADD46545	ADD46545 Human pro
40	52	53.6	733	6	ADA34312	ADA34312 Acinetoba
41	51.5	53.1	20	5	ABP46756	ABP46756 Human BLY
42	51.5	53.1	101	2	RAY37253	RAY37253 Protein w
43	51.5	53.1	256	5	ABP45290	ABP45290 Human BLY
44	50.5	52.1	36	2	AAW03964	AAW03964 VDJ joint
45	50.5	52.1	36	2	AAW41127	AAW41127 VH251 DXF

ALIGNMENTS

RESULT 1
AAE37203
ID AAE37203 standard; protein; 143 AA.

XX AAE37203;
DT 07-AUG-2003 (first entry)
DE Human AB-PQ1-XG1-026 PSMA antibody heavy chain variable region (VH).
KW Human; Prostate specific membrane antigen; carcinoma; sarcoma; cancer;
KW PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase;
KW folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase;
KW NAALADase; antibody; heavy chain variable region; VH.

OS Homo sapiens.

XX WO2003034903-A2.

XX 01-MAY-2003.

XX 23-OCT-2002; 2002WO-US033944.

XX 23-OCT-2001; 2001US-0335215P.

XX 07-MAR-2002; 2002US-0362747P.

XX 20-SEP-2002; 2002US-0412618P.

XX (PSMA-) PSMA DEV CO LLC.

XX Maddon PJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;

XX WPI; 2003-403281/38.

XX N-PSDB; AAD56218.

XX Novel isolated antibody which binds to epitope on prostate specific membrane antigen, and competitively inhibits binding of second antibody to its target epitope on the antigen, useful for treating prostate cancer.

XX Claim 26; Page 229-230; '238pp; English.

XX The invention relates to an antibody or its antigen-binding fragment which specifically binds to epitope on prostate specific membrane antigen (PSMA), and competitively inhibits the specific binding of a second antibody to its target epitope on PSMA. The invention is useful for diagnosing, treating or preventing PSMA-mediated disease such as prostate cancer or non-prostate cancer bladder chosen from cancer including transitional cell carcinoma, pancreatic cancer including pancreatic duct

CC carcinoma, lung cancer including non-small cell lung carcinoma, kidney
 CC cancer including conventional renal cell carcinoma, sarcoma including
 CC soft tissue sarcoma, breast cancer including breast carcinoma, brain
 CC cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon
 CC cancer including colonic carcinoma, testicular cancer including
 CC testicular embryonal carcinoma, or melanoma including malignant melanoma.
 CC The invention is useful also for inhibiting or enhancing folate hydrolase
 CC activity of a folate hydrolase polypeptide, N-acetylated alpha-linked
 CC acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide,
 CC dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase IV
 CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl
 CC hydrolase polypeptide. The present sequence is human PSMA antibody heavy
 CC chain variable region (VH)
 XX SQ Sequence 143 AA;
 Query Match 64.4%; Score 62.5; DB 6; Length 143;
 Best Local Similarity 73.3%; Pred. No. 0.23;
 Matches 11; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
 Qy 3 GYSVNDY-YGMDV 16
 Db 118 GYNWNEYHYXGMDV 132
 RESULT 2
 ID AAMS1172 standard; protein; 146 AA.
 XX AC AAMS1172;
 XX 10-JUN-2002 (first entry)
 XX Human recombinant mAb TNV196 heavy chain variable region.
 XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
 KW complementarity determining region; antirheumatic; antiarthritic;
 KW antidiabetic; antiallergic; antiinflammatory; antischlicking;
 KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;
 KW antidiabetic; cardiatic; antibacterial; virucide; fungicide; antileprotic;
 KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
 KW human; diagnosis; therapy; TNV196; monoclonal antibody; mAb.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /label= Signal_peptide
 FT /note= "amino acids 1-7 are PCR primer-encoded and may
 FT differ from the native sequence"
 FT 20..146
 FT Protein /label= Mature_protein
 FT 31..49
 FT Region /label= FR1
 FT 50..54
 FT Region /label= CDR1
 FT 55..68
 FT Region /label= FR2
 FT 69..85
 FT Region /label= CDR2
 FT 86..117
 FT Region /label= FR3
 FT 118..135
 FT Region /label= CDR3
 FT 126
 FT Misc-difference /note= "encoded by A"
 FT 136..146
 FT Region /label= J6
 XX WO200212502-A2.
 XX 14-FEB-2002.

PF 07-AUG-2001; 2001WO-US024785.
 XX 07-AUG-2000; 2000US-0223360P.
 PR 29-SEP-2000; 2000US-0236826P.
 PR 01-AUG-2001; 2001US-00920137.
 XX (CENZ) CENTOCOR INC.
 PA Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
 XX WPI; 2002-217194/27.
 DR N-PSDB; ABL53512.
 XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
 PT angina pectoris, myocardial infarction, leprosy.
 XX Example 3; Fig 4; 131pp; English.
 XX The present sequence is that of the heavy chain variable region of anti-
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
 CC TNV196. TNV196 was 1 of 8 human mAbs produced from a GentV fusion using
 CC spleen cells from a hybrid mouse containing human variable and constant
 CC region antibody transgenes that was immunised with human TNF alpha. The
 CC human mAbs bound immobilised human TNF alpha with high avidity and had a
 CC totally human IgG1, kappa isotype. They showed relatedness to each other
 CC and to the human germline DP-46 heavy chain sequence (see AAMS1167). The
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,
 CC humanised and/or complementarity determining region (CDR)-grafted anti-
 CC TNF antibodies, immunoglobulins, cleavage products and other specified
 CC portions and variants, as well as anti-TNF antibody compositions,
 CC encoding or complementary nucleic acids, vectors, host cells,
 CC compositions, formulations, devices, transgenic animals, transgenic
 CC plants, and methods of making and using them. The anti-TNF antibody
 CC comprises at least a portion of an immunoglobulin molecule, especially
 CC the heavy chain and/or light chain variable regions given in the present
 CC sequence and in AAMS1165, or either all of the CDRs of the heavy chain
 CC (see AAMS1158-60) or all of the CDRs of the light chain (see AAMS1161-
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
 CC in a mouse model. They are useful for diagnosing or treating a TNF
 CC related condition in a cell, tissue, organ or animal (claimed) such as
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
 CC myocardial infarction, an infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
 CC Creutzfeldt-Jakob disease
 XX SQ Sequence 146 AA;
 Query Match 60.8%; Score 59; DB 5; Length 146;
 Best Local Similarity 68.8%; Pred. No. 0.76;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 GFGVSYNDYVYXGMDV 16
 Db 120 GIGAGNYYVYVXGMDV 135
 RESULT 3
 ID ABR41574 standard; protein; 112 AA.
 XX ABR41574;
 XX 02-JUN-2003 (first entry)
 XX Human DITHP antigen recognition protein.

KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; genotyping; transcript imaging;
 KW antigen recognition.
 XX
 OS Homo sapiens.
 XX
 FN WO200297031-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 27-MAR-2002; 2002WO-US010056.
 XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 15-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Anshey SR;
 PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 XX WPI; 2003-129518/12.
 DR N-PSDB; ACC46512.
 DR
 XX
 XX Novel human diagnostic and therapeutic polypeptide useful for identifying
 PT test compound which specifically binds to a polypeptide encoded by human
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
 XX
 XX Claim 27; SEQ ID NO 1109; 591pp; English.
 XX
 XX The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
 CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
 CC polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
 CC detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which has antigen
 CC recognition activity. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 112 AA;
 SQ
 Query Match 58.8%; Score 57; DB 6; Length 112;
 Best Local Similarity 71.4%; Pred. No. 1.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GYSYNDYYGMDV 16
 DB 45 GYDGYVYVYGMV 58
 RESULT 4
 ABP46758
 ID ABP46758 standard; peptide; 21 AA.
 XX
 AC ABP46758;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv VH CDR3 SEQ ID 2769.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US019110.
 XX
 XX 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 PS
 Claim 2; Page 3048; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

SQ Sequence 21 AA;

Query Match 58.2%; Score 56.5; DB 5; Length 21;
 Best Local Similarity 78.6%; Pred. No. 0.21;
 Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 GYSYNDYDYYGMDV 16
 |||:|||||
 DB 9 GY-YLWDYDYYGMDV 21

RESULT 5
 ABP45542
 ID ABP45542 standard; protein; 257 AA.
 XX
 AC ABP45542;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 1553.
 XX
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 FI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 diagnosis and treatment of cancers and immune disorders.
 PS Claim 1; Page 2256-2257; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 tumour necrosis factor (TNF) super family and induces B cell
 proliferation and differentiation. The antibodies of the invention have
 cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 antirheumatic and antiAIDS activity and can be used in vaccines to
 inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 and so may be used to detect and quantitate the presence of BlyS in
 biological samples and may be used in this way to diagnose disease
 associated with aberrant expression of BlyS. They may also be
 administered to treat diseases associated with aberrant BlyS expression
 and activity such as cancer, immune, and autoimmune disorders and
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 the antibodies and fragments of the antibodies described in the method of
 the invention
 XX
 SQ Sequence 257 AA;

Query Match 58.2%; Score 56.5; DB 5; Length 257;
 Best Local Similarity 78.6%; Pred. No. 3.2;
 Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 GYSYNDYDYYGMDV 16
 |||:|||||
 DB 107 GY-YLWDYDYYGMDV 119

RESULT 6
 ABG77138
 ID ABG77138 standard; protein; 124 AA.
 XX
 AC ABG77138;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Anti-IGF-IR antibody (2.13.2) variable region heavy chain protein.
 XX
 KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
 KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;
 KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
 KW acromegaly; gigantism; psoriasis; atherosclerosis.
 OS Homo sapiens.
 XX
 PN WO200253596-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-US051113.
 XX
 PR 05-JAN-2001; 2001US-0259927P.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX
 DR WPI; 2002-575410/61.
 DR N-PSDB; ABS62700.
 XX
 PT Novel humanized, chimeric monoclonal antibody that specifically binds to
 insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
 PS Claim 13; Page 127; 172pp; English.
 XX
 CC This invention relates to a novel humanised, chimeric or human monoclonal
 antibody or its antigen binding portion that specifically binds to
 insulin-like growth factor I receptor (IGF-IR). The antibodies of the
 invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
 IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 phosphorylation. The antibodies of the invention are useful for
 diagnosing the presence or location of an IGF-IR-expressing tumour in a
 subject. The antibody or its antigen-binding portion is also useful for
 treating cancer in a human. The method for this further involves an anti
 neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
 antibodies may also be useful for increasing IGF-IR activity and thus
 restoring IGF-IR activity in a condition characterised by low IGF-IR
 levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
 also useful for inducing apoptosis of specific cells in a patient, and to
 treat non-cancerous states or disease, e.g. acromegaly, gigantism,
 psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
 minimise the immunogenic and allergic responses intrinsic to mouse or
 mouse-derived monoclonal antibodies and thus increase the efficacy
 and safety of the administered antibodies. The present sequence
 represents an anti-insulin-like growth factor I receptor antibody of the
 invention
 XX
 SQ Sequence 124 AA;

Query Match 57.7%; Score 56; DB 5; Length 124;
 Best Local Similarity 71.4%; Pred. NO. 1.7;
 Matches 10; Conservative 2; Mismatches 0; Gaps 0;

QY 3 GYSYNDYDYYGMDV 16
 Db 100 GMSDSYDYYGMDV 113

RESULT 7
 AAM79672
 ID AAM79672 standard; protein; 170 AA.

XX AC AAM79672;
 XX DT
 XX DE 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 3318.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.
 XX PN WO200157190-A2.
 XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.
 XX PR 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PR 20-JUN-2000; 2000US-00598075.
 XX PR 19-JUL-2000; 2000US-00620325.
 XX PR 01-SEP-2000; 2000US-00654936.
 XX PR 15-SEP-2000; 2000US-00663561.
 XX PR 20-OCT-2000; 2000US-00693325.
 XX PR 30-NOV-2000; 2000US-00728422.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX DR WPI; 2001-476283/51.
 XX DR N-PSDB; AAK52805.

XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 XX in diagnosis and gene therapy.

XX PS Claim 20; Page 306; 6221pp; English.

XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX SQ Sequence 170 AA;

Query Match 57.7%; Score 56; DB 4; Length 170;
 Best Local Similarity 72.7%; Pred. NO. 2.4;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 YSYNDYDYYGM 14
 Db 16 YNYGFDYDYYGM 26

RESULT 8

AAM24101
 ID AAM24101 standard; protein; 384 AA.

XX AC AAM24101;

XX DT 12-OCT-2001 (first entry)

XX DE Human EST encoded protein SEQ ID NO: 1626.

XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.

XX OS Homo sapiens.

XX PN WO200154477-A2.

XX PD 02-AUG-2001.

XX PF 25-JAN-2001; 2001WO-US002687.

XX PR 25-JAN-2000; 2000US-00491404.

XX PR 17-JUL-2000; 2000US-00617746.

XX PR 03-AUG-2000; 2000US-00631451.

XX PR 15-SEP-2000; 2000US-00663870.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX DR WPI; 2001-476164/51.

XX DR N-PSDB; AAK98760.

XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 XX antibodies and research use.

XX PS Claim 20; Page 1102-1103; 1275pp; English.

XX CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention

XX SQ Sequence 384 AA;

Query Match 57.7%; Score 56; DB 4; Length 384;
 Best Local Similarity 76.9%; Pred. NO. 5.9;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YSYNDYDYYGMDV 16

Db 129 YSSHYDYYGMDV 141

RESULT 9

ABG77157
 ID ABG77157 standard; protein; 470 AA.

XX ABG77157;

XX		24-OCT-2002	(first entry)	
DT				
XX		Amino acid sequence of anti-IGF-IR antibody 2.13.2 Vh domain.		
DE				
XX				
KW		Insulin-like growth factor I receptor; antibody; human; cytostatic;		
KW		osteopathic; antithrombotic; anticancer; IGF-IR; tumour;		
KW		anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;		
XX		acromegaly; gigantism; psoriasis; atherosclerosis.		
XX				
OS		Homo sapiens.		
XX				
PN		WO200253596-A2.		
PD				
XX		11-JUL-2002.		
PP		20-DEC-2001; 2001WO-US051113.		
PR		05-JAN-2001; 2001US-0259927P.		
XX		(PFIZ) PFIZER INC.		
PA		(ABGE-) AGENIX INC.		
XX				
PI		Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;		
XX				
DR		WPI; 2002-575410/51.		
XX				
PT		Novel humanized, chimeric monoclonal antibody that specifically binds to		
PT		insulin-like growth factor I (IGF-I) receptor useful for inhibiting		
PT		binding of IGF-I or IGF-II to receptor and for treating cancer in humans.		
XX				
PS		Claim 16; Fig 19B; 172pp; English.		
XX				
CC		This invention relates to a novel humanised, chimeric or human monoclonal		
CC		antibody or its antigen binding portion that specifically binds to		
CC		insulin-like growth factor I receptor (IGF-IR). The antibodies of the		
CC		invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-		
CC		IR and can inhibit in vivo tumour growth and IGF-IR tyrosine		
CC		phosphorylation. The antibodies of the invention are useful for		
CC		diagnosing the presence or location of an IGF-IR-expressing tumour in a		
CC		subject. The antibody or its antigen-binding portion is also useful for		
CC		treating cancer in a human. The method for this further involves an anti		
CC		neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The		
CC		antibodies may also be useful for increasing IGF-IR activity and thus		
CC		restoring IGF-IR activity in a condition characterised by low IGF-IR		
CC		levels e.g. neuropathy, or osteoporosis. An antibody of the invention is		
CC		also useful for inducing apoptosis of specific cells in a patient, and to		
CC		treat non-cancerous states or disease, e.g. acromegaly, gigantism,		
CC		psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies		
CC		minimise the immunogenic and allergic responses intrinsic to mouse or		
CC		mouse-derived monoclonal antibodies and thus increase the efficacy		
CC		and safety of the administered antibodies. The present sequence		
CC		represents an anti-insulin-like growth factor I receptor antibody of the		
CC		invention		
XX				
SQ		Sequence 470 AA;		
		Query Match	57.7%; Score 56; DB 5; Length 470;	
		Best Local Similarity	71.4%; Pred. No. 7, 4;	
		Matches 10; Conservative	2; Mismatches 2; Indels 0; Gaps	
Qy		3 GYSNYDYYYGMDV 16		
		:		
Db		120 GWSDSYYYGYMDV 133		
		RESULT 10		
		RAM78698		
ID		AAW78688 standard; protein; 590 AA.		
XX				
AC		AAW78688;		
XX				
DT		06-NOV-2001 (first entry)		

XX Human; immune response; chronic B-lymphoproliferative disorder; CDR3;
KW complementarity determining region 3; hypervariable region; B-cell;
KW immunoglobulin heavy chain; VH-CDR3; idiotypic immunoglobulin;
KW cytototoxic; hairy cell leukaemia.
XX
OS Homo sapiens.
XX
PN WO200255559-A1.
XX
PD 18-JUL-2002.
XX
PF 15-JAN-2001; 2001WO-IT000014.
XX
PR 15-JAN-2001; 2001WO-IT000014.
XX
PA (FAZI/) FAZIO V M.
PA (SAGL/) SAGLIO G.
XX
XX Fazio VM, Saglio G;
XX NPI; 2002-583654/62.
XX
DR N-PSDB; ABK90003.
XX
XX Use of DNA sequences coding for hypervariable region (VH- complementarity
PT determining region 3 (CDR3)) of idiotypic immunoglobulin expressed on B-
PT cells of chronic B- lymphoproliferative disorders, as therapeutic
PT vaccine.
XX
XX Disclosure; Fig 2; 30pp; English.
XX
XX The present invention relates to a method for inducing an immune response
CC against B-lymphoproliferative disorders. The method comprises DNA
CC sequences encoding for the complementarity determining region 3 (CDR3)
CC hypervariable region of immunoglobulin heavy chain (VH-CDR3) alone or in
CC combination with at least another immunomodulating sequence. The DNA
CC sequences are useful as therapeutic vaccines for chronic B-
CC lymphoproliferative disorders in mammals, preferably humans. A
CC recombinant plasmid expression vector containing a DNA sequence of the
CC invention is useful as a therapeutic vaccine or for the manufacture of a
CC vaccine effective against chronic B-lymphoproliferative disorders
CC expressing the surface idiotypic immunoglobulin on B-cells in mammals,
CC preferably humans. An efficient, safe and easily reproducible DNA-based
CC immune response against B-lymphoproliferative pathologies can be
CC achieved. The present sequence representing human CDR3 variable region is
CC isolated from a hairy cell leukaemia patient
XX
SQ Sequence 44 AA;
Query Match 56.7%; Score 55; DB 5; Length 44;
Best Local Similarity 76.9%; Pred. NO. 0.76;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 4 YSYNDYDYYGMDV 16
DB 21 YISNYYYGMDV 33
RESULT 12
ADA89202
ID ADA89202 standard; protein; 128 AA.
XX
AC ADA89202;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.
XX
XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytototoxic; Gene therapy; cancerous disorder;
KW cancer.
XX

OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070752-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005128.
XX
PR 20-FEB-2002; 2002US-0358994P.
XX
PA (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Hoogenboom HRJM, Reiter Y;
PI WPI; 2003-663847/62.
DR N-PSDB; ADA89201.
XX
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
XX Disclosure; Fig 10B; 224pp; English.
XX
XX The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. ALSO described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC gp100.
XX
SQ Sequence 128 AA;
Query Match 56.7%; Score 55; DB 6; Length 128;
Best Local Similarity 83.3%; Pred. NO. 2.5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 5 SYNDYDYYGMDV 16
DB 106 SYPYYYGMDV 117
RESULT 13
ABP57367
ID ABP57367 standard; protein; 145 AA.
XX
XX ABP57367;
XX
XX 22-APR-2003 (first entry)
XX
XX Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.
XX

KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
 KW antibody therapy.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200294880-A1.
 XX 28-NOV-2002.
 XX 17-MAY-2002; 2002WO-JP004816.
 XX 18-MAY-2001; 2001JP-00150213.
 PR 09-AUG-2001; 2001JP-00243040.
 PR 11-OCT-2001; 2001JP-00314489.
 XX (KIRI) KIRIN BEER KK.
 XX Mori E, Kataoka S;
 XX WPI; 2003-120790/11.
 DR N-PSDB; ABZ59698.
 XX New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
 PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
 PT nor inducing injury to hepatocytes, for use in therapy of malignant
 PT tumor.
 XX Claim 54; Page 62; 92pp; Japanese.
 PS The present invention describes antibodies or their functional fragments
 XX that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
 CC have cytostatic and apoptotic activities, and can be used in antibody
 CC therapy. The antibodies can be applied as remedies and preventives of
 CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
 CC in the therapy of malignant tumours. Remedies produced with the
 CC antibodies are highly safe, and avoid hepatotoxicity. The present
 CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
 XX present invention
 XX Sequence 145 AA;
 SQ Query Match 56.7%; Score 55; DB 6; Length 145;
 Best Local Similarity 83.3%; Pred. No. 2.8;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 SYNDYDYYGMDV 16
 DB 123 SYRDYDYYGMDV 134
 RESULT 14
 ID ABO04856
 XX ABO04856 standard; protein; 157 AA.
 AC ABO04856;
 XX 12-AUG-2003 (first entry)
 DT Human epidermal growth factor receptor (EGF-r) antibody #29.
 DE Human; epidermal growth factor receptor; EGF-r; antibody; cytostatic;
 XX antiinflammatory; immunosuppressive; tyrosine phosphorylation; EGF-2;
 KW EGF-r degradation; vascular endothelial cell growth factor; VEGF; tumour;
 XX endothelial cell; threonine phosphorylation; autoimmune disease; colon;
 XX inflammation; lung; cancer.
 OS Homo sapiens.
 XX US2002173629-A1.
 PN 21-NOV-2002.
 XX

PF 05-NOV-1998; 98US-00187693.
 XX 05-MAY-1997; 97US-00851362.
 PR 29-SEP-1998; 98US-00162280.
 XX (JAKO/) JAKOBOWITS A.
 PA (YANG/) YANG X.
 PA (GALL/) GALLO M.
 PA (JIA/) JIA X.
 XX Jakobovits A, Yang X, Gallo M, Jia X;
 PI WPI; 2003-328430/31.
 DR N-PSDB; ACD10940.
 XX Fully human monoclonal antibodies that bind to epidermal growth factor
 PT receptors, useful in cancer therapy.
 XX Example 3; Fig 69; 100pp; English.
 XX The invention relates to an antibody that binds to an epidermal growth
 CC factor receptor (EGF-r) and exhibits inhibition of tyrosine
 CC phosphorylation of EGF-2, the degradation of EGF-r, the EGF induced
 CC degradation of EGF-r, vascular endothelial cell growth factor (VEGF)
 CC production by tumour cells (by greater than 50%) and endothelial cells
 CC (by greater than 40%) and also protects threonine phosphorylation of EGF-
 CC r and a 63KD protein. The antibody is internalised with EGF-r. The
 CC antibody may be used for treating tumours such as lung tumours and colon
 CC tumours and for treating inflammation and autoimmune diseases. Sequences
 CC ABO04824-ABO04859 represent human EGF-r receptor antibodies of the
 CC invention
 XX Sequence 157 AA;
 SQ Query Match 55.7%; Score 54; DB 6; Length 157;
 Best Local Similarity 64.3%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GYSYNDYDYYGMDV 16
 DB 87 GOKWSYDYYGMDV 100
 RESULT 15
 ID AAU70375 standard; peptide; 18 AA.
 XX AAU70375;
 XX 14-FEB-2002 (first entry)
 DT Mouse heavy chain I CDR 3.
 DE Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 XX complementarity determining region; framework region; IGBP;
 KW transgenic plant; immunoglobulin binding protein array; IGM; IGA; IGA;
 KW IGD; IGE; IGV; IGM; kappa; lambda; CHBP.
 XX Mus musculus.
 OS WO200183806-A1.
 XX 08-NOV-2001.
 PD 02-MAY-2001; 2001WO-US014349.
 PF 02-MAY-2000; 2000US-00563222.
 XX (EPIC-) EPICYTE PHARM INC.
 XX Hiatt AC, Hein MB;
 PI WPI; 2002-055482/07.
 DR

XX Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Page 15; 129pp; English.
XX
XX The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds to
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 18 AA;

Query Match 55.2%; Score 53.5; DB 5; Length 18;
Best Local Similarity 62.5%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 GFGYS-YNYDYGGMD 15
|:| | | | | |
Db 2 GYGYYDYDYFFD 17

Search completed: April 21, 2004, 17:33:12
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 48.2319 Seconds

(without alignments)
91.715 Million cell updates/sec

Title: SEQ3

Perfect score: 97

Sequence: 1 gfgysnydydygmav 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	125	14	US-10-041-860-48
2	97	100.0	125	14	US-10-041-860-200
3	97	100.0	125	14	US-10-041-860-237
4	97	100.0	125	14	US-10-041-860-372
5	83	85.6	125	14	US-10-041-860-38
6	83	85.6	125	14	US-10-041-860-203
7	83	85.6	125	14	US-10-041-860-240
8	83	85.6	125	14	US-10-041-860-343
9	62.5	64.4	143	12	US-10-395-894-19
10	59.5	61.3	126	14	US-10-041-860-25
11	59.5	61.3	126	14	US-10-041-860-210
12	59.5	61.3	126	14	US-10-041-860-246
13	59.5	61.3	126	14	US-10-041-860-306
14	56.5	58.2	21	10	US-09-880-748-2769
15	56.5	58.2	21	12	US-10-293-418-2769

16	56.5	58.2	257	10	US-09-880-748-1553	Sequence 1553, Ap
17	56.5	58.2	257	12	US-10-293-418-1553	Sequence 1553, Ap
18	55	56.7	128	12	US-10-371-942-46	Sequence 46, Appl
19	54	55.7	157	9	US-09-187-693-67	Sequence 67, Appl
20	53.5	55.2	18	10	US-09-563-222-55	Sequence 55, Appl
21	53	54.6	19	10	US-09-880-748-2387	Sequence 2387, Ap
22	53	54.6	19	12	US-10-293-418-2387	Sequence 2387, Ap
23	53	54.6	254	10	US-09-880-748-1625	Sequence 1625, Ap
24	53	54.6	254	12	US-10-293-418-1625	Sequence 1625, Ap
25	52.5	54.1	24	10	US-09-880-748-2926	Sequence 2926, Ap
26	52.5	54.1	24	12	US-10-293-418-2926	Sequence 2926, Ap
27	52.5	54.1	145	12	US-10-395-894-23	Sequence 23, Appl
28	52.5	54.1	260	10	US-09-880-748-1458	Sequence 1458, Ap
29	52.5	54.1	260	12	US-10-293-418-1458	Sequence 1458, Ap
30	52	53.6	17	10	US-09-880-748-2836	Sequence 2836, Ap
31	52	53.6	17	12	US-10-293-418-2836	Sequence 2836, Ap
32	52	53.6	19	10	US-09-880-748-2735	Sequence 2735, Ap
33	52	53.6	19	12	US-10-293-418-2735	Sequence 2735, Ap
34	52	53.6	24	9	US-09-891-064A-4	Sequence 4, Appl
35	52	53.6	252	10	US-09-880-748-1415	Sequence 1415, Ap
36	52	53.6	252	12	US-10-293-418-1415	Sequence 1415, Ap
37	52	53.6	254	10	US-09-880-748-1259	Sequence 1259, Ap
38	52	53.6	254	12	US-10-293-418-1259	Sequence 1259, Ap
39	52	53.6	255	10	US-09-880-748-1271	Sequence 1271, Ap
40	52	53.6	255	12	US-09-880-748-1284	Sequence 1284, Ap
41	52	53.6	255	12	US-10-293-418-1271	Sequence 1271, Ap
42	52	53.6	255	12	US-10-293-418-1284	Sequence 1284, Ap
43	52	53.6	257	10	US-09-880-748-1283	Sequence 1283, Ap
44	52	53.6	257	12	US-10-293-418-1283	Sequence 1283, Ap
45	52	53.6	522	9	US-09-891-064A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-041-860-48
; Sequence 48, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvelan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-48

Query Match 100.0%; Score 97; DB 14; Length 125;
Best Local Similarity 100.0%; Pred.No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYSNYDYDYGMV 16
|||
DB 99 GFGYSNYDYDYGMV 114

RESULT 2
US-10-041-860-200
; Sequence 200, Application US/10041860

Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 200
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-200

Query Match 100.0%; Score 97; DB 14; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYYGMDV 16
 |||||
 Db 99 GFGYSYNDYYGMDV 114

RESULT 3
 US-10-041-860-237
 ; Sequence 237, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 237
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-237

Query Match 100.0%; Score 97; DB 14; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYYGMDV 16
 |||||
 Db 99 GFGYSYNDYYGMDV 114

RESULT 4
 US-10-041-860-372
 ; Sequence 372, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong

APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 372
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-372

Query Match 100.0%; Score 97; DB 14; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYYGMDV 16
 |||||
 Db 99 GFGYSYNDYYGMDV 114

RESULT 5
 US-10-041-860-38
 ; Sequence 38, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-38

Query Match 85.6%; Score 83; DB 14; Length 125;
 Best Local Similarity 87.5%; Pred. No. 0.00029;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYYGMDV 16
 |||||
 Db 99 GSGYSYDYYGMDV 114

RESULT 6
 US-10-041-860-203
 ; Sequence 203, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-203

Query Match 85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYIYGMVDV 16
Db 99 GSGYSYGYDIYGMVDV 114

RESULT 7
US-10-041-860-240
; Sequence 240, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-240

Query Match 85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYIYGMVDV 16
Db 99 GSGYSYGYDIYGMVDV 114

RESULT 8
US-10-041-860-343
; Sequence 343, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343

Query Match 85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYSYNDYIYGMVDV 16
Db 99 GSGYSYGYDIYGMVDV 114

RESULT 9
US-10-395-894-19
; Sequence 19, Application US/10395894
; Publication No. US2004003229A1
; GENERAL INFORMATION:
; APPLICANT: MADDON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHLKE, No. US2004003229A1bert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA, Dangshe
; TITLE OF INVENTION: FSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCT/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/412,618
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-395-894-19

Query Match 64.4%; Score 62.5; DB 12; Length 143;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 3 GYSYNDY-YIYGMVDV 16
Db 118 GYNWYEVHYIYGMVDV 132

RESULT 10
US-10-041-860-25
; Sequence 25, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine

```

; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-25

```

```

Query Match      61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

QY      3 GYSYNYDY-YGMDV 16
      ||||| |||||
DB      101 GYSYGYVYDYGMDV 115

```

```

RESULT 11
US-10-041-860-210
; Sequence 210, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-210

```

```

Query Match      61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

QY      3 GYSYNYDY-YGMDV 16
      ||||| |||||
DB      101 GYSYGYVYDYGMDV 115

```

```

RESULT 12
US-10-041-860-246
; Sequence 246, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam

```

```

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-246

```

```

Query Match      61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

QY      3 GYSYNYDY-YGMDV 16
      ||||| |||||
DB      101 GYSYGYVYDYGMDV 115

```

```

RESULT 13
US-10-041-860-306
; Sequence 306, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-306

```

```

Query Match      61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

QY      3 GYSYNYDY-YGMDV 16
      ||||| |||||
DB      101 GYSYGYVYDYGMDV 115

```

```

RESULT 14
US-09-880-748-2769
; Sequence 2769, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

```

; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2769
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2769

Query Match 58.2%; Score 56.5; DB 10; Length 21;
Best Local Similarity 78.6%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 3 GYSYNDYVYGMV 16
|||:|||||||
Db 9 GY-YLWDYVYGMV 21

RESULT 15
US-10-293-418-2769
; Sequence 2769, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/275,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2769
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2769

Query Match 58.2%; Score 56.5; DB 12; Length 21;
Best Local Similarity 78.6%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 3 GYSYNDYVYGMV 16
|||:|||||||
Db 9 GY-YLWDYVYGMV 21

Search completed: April 21, 2004, 18:02:06
Job time : 49.2319 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 8.11594 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: SEQ3
Perfect score: 97
Sequence: 1 gfgysynydygmdv 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	57.7	591	1	ARSF_HUMAN
2	52	53.6	522	1	OCNL_HUMAN
3	52	53.6	733	1	PTK_ACIJO
4	50	51.5	733	1	HXA_BIADI
5	49	50.5	59	1	CUTB_LIMPO
6	48	49.5	146	1	HV21_HUMAN
7	48	49.5	312	1	RV1_MOUSE
8	48	49.5	521	1	OCNL_CANFA
9	47	48.5	504	1	OCNL_CHICK
10	47	48.5	719	1	FRB4_YEAST
11	47	48.5	1048	1	YCB1_METUA
12	46	47.4	201	1	YK00_YEAST
13	46	47.4	633	1	ROR_HUMAN
14	46	47.4	646	1	NA95_HUMAN
15	45	46.4	321	1	VG74_HVSA
16	45	46.4	394	1	OM51_SALTI
17	45	46.4	397	1	YBDS_ECOLI
18	45	46.4	1312	1	DPOL_PPRSD
19	44.5	45.9	435	1	YBBO_BACSU
20	44.5	45.9	722	1	Y006_KLEPN
21	44.5	45.9	1326	1	BCC2_ACEXY
22	44	45.4	59	1	CUT7A_LIMPO
23	44	45.4	59	1	CUT7C_LIMPO
24	44	45.4	147	1	HVLC_HUMAN
25	44	45.4	183	1	DERM_BOVIN
26	44	45.4	201	1	DERM_HUMAN
27	44	45.4	631	1	ADAS_DROME
28	44	45.4	642	1	NA95_MOUSE
29	44	45.4	772	1	LP1G_DROME
30	44	45.4	789	1	LP1A_DROME
31	43.5	44.8	726	1	AMSA_ERWAN
32	43.5	44.8	1302	1	ACSC_ACEXY
33	43	44.3	316	1	Y034_METUA

34	43	44.3	667	1	EM70_YEAST
35	42	43.3	214	1	YB41_METUA
36	42	43.3	306	1	RALY_HUMAN
37	42	43.3	369	1	OMPP_YENNE
38	42	43.3	461	1	FUCO_DICDI
39	42	43.3	687	1	AKA8_RAT
40	42	43.3	826	1	VILI_CHICK
41	41.5	42.8	330	1	SLEB_BACHD
42	41.5	42.8	429	1	AST1_YEAST
43	41.5	42.8	1325	1	BCC3_ACEXY
44	41	42.3	102	1	YAS9_HAEIN
45	41	42.3	130	1	C14A_LIMPO

ALIGNMENTS

RESULT 1					
ARSF_HUMAN					
ID	ARSF_HUMAN	STANDARD;	PRT;	591	AA.
AC	P54793;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Arylsulfatase F precursor (EC 3.1.6.-) (ASF).				
GN	ARSF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=97336043; PubMed=9192838;				
RA	Puca A.A., Zolli M., Repetto M., Andolfi G., Guffanti A., Simon G.,				
RA	Ballabio A., Franco B.;				
RT	"Identification by shotgun sequencing, genomic organization, and				
RT	functional analysis of a fourth arylsulfatase gene (ARSF) from the				
RT	Xp22.3 region."				
RL	Genomics 42:192-199(1997).				
RN	[2]				
RP	SEQUENCE OF 370-423 FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=95236447; PubMed=7720070;				
RA	Franco B., Meroni G., Parenti G., Leveilliers J., Bernard L.,				
RA	Gebbia M., Cox L., Maroteaux P., Sheffield L., Rappold G.A.,				
RA	Andria G., Petit C., Ballabio A.;				
RT	"A cluster of sulfate genes on Xp22.3: mutations in				
RT	chondrodysplasia punctata (CDPX) and implications for warfarin				
RT	embryopathy."				
RL	Cell 81:15-25(1995).				
CC	-I- ENZYME REGULATION: Not inhibited by DHEAS or warfarin.				
CC	-I- MISCELLANEOUS: Optimum pH is 8.				
CC	-I- SIMILARITY: Belongs to the sulfatase family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; X97868; CAA66462.1; -.				
DR	PIR; A56217; A56217.				
DR	HSSP; P15848; 1FSU.				
DR	Genew; HGNC:721; ARSF.				
DR	MIM; 300003; -.				
DR	GO; GO:0004085; P:arylsulfatase activity; TAS.				
DR	InterPro; IPR000917; Sulfatase.				
DR	Pfam; PF00884; Sulfatase; 1.				
DR	PROSITE; PS00523; SULFATASE_1; 1.				
DR	PROSITE; PS00149; SULFATASE_2; 1.				

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KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 591 ARYL SULFATASE F.
FT MOD_RES 79 79 2-AMINO-3-OXOPROPIONIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 140 140 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 591 AA; 66003 MW; 85B4EBF3803A771 CRC64;

Query Match 57.7%; Score 56; DB 1; Length 591;
Best Local Similarity 72.7%; Pred. No. 0.85;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSYNYDYDYYG 14
Db 156 YNYGFDYYG 166

RESULT 2
OCLN_HUMAN STANDARD; PRT; 522 AA.
ID Q16625; Q8NEK1;
AC Q16625; Q8NEK1;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Occludin.
GN OCLN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon carcinoma;
RX MEDLINE=96181088; PubMed=8601611;
RA Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,
RA Itoh M., Yonemura S., Furuse M., Tsukita S.;
RT "Interspecies diversity of the occludin sequence: cDNA cloning of
RT human, mouse, dog, and rat-kangaroo homologues.";
RL J. Cell Biol. 133:43-47(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA van Itallie C.M., Fanning A.S., Anderson J.M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Fukasawa M., Toyota T., Yoshitsugu K., Yoshikawa T.;
RT "Genomic structure of occludin gene.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

-!- FUNCTION: May play a role in the formation and regulation of the tight junction (TJ) paracellular permeability barrier.

-!- SUBUNIT: Interacts with TJPI/ZOI and with VAPA.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells. Highly expressed in kidney.

Not detected in testis.

-!- DOMAIN: The C-terminal is cytoplasmic and is important for interaction with ZO-1. Sufficient for the tight junction localization. Involved in the regulation of the permeability barrier function of the tight junction (By similarity).

-!- PTM: Phosphorylated (By similarity).

-!- SIMILARITY: Belongs to the ELL / Occludin family.

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EMBL; U49184; AAC50451.1; -;
EMBL; U53823; AB000195.1; -;
EMBL; AF400630; AAL47094.1; -;
EMBL; AF400623; AAL47094.1; JOINED.
EMBL; AF400624; AAL47094.1; JOINED.
EMBL; AF400625; AAL47094.1; JOINED.
EMBL; AF400626; AAL47094.1; JOINED.
EMBL; AF400627; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; AF400629; AAL47094.1; JOINED.
EMBL; AF400630; AAL47094.1; JOINED.
EMBL; BC029886; AAH29886.1; -;
PIR; G02533; G02533.
Genew; HGNC:8104; OCLN.
MIM; 602875; -;
CO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005463; P:protein complex assembly; TAS.
InterPro; IPR008253; Marvel.
InterPro; IPR002958; Occludin.
Pfam; PF01284; MARVEL; 1.
PRINTS; PR01258; OCLUDIN.
Tight junction; Transmembrane; Coiled coil; Phosphorylation.
DOMAIN 1 66 CYTOPLASMIC (POTENTIAL).
TRANSMEM 67 89 EXTRACELLULAR (POTENTIAL).
DOMAIN 90 135 POTENTIAL.
TRANSMEM 136 160 CYTOPLASMIC (POTENTIAL).
DOMAIN 161 170 POTENTIAL.
TRANSMEM 171 195 EXTRACELLULAR (POTENTIAL).
DOMAIN 196 243 POTENTIAL.
TRANSMEM 244 265 CYTOPLASMIC (POTENTIAL).
DOMAIN 266 522 TYR/GLY-RICH.
DOMAIN 92 131 COILED COIL (POTENTIAL).
DOMAIN 426 489 COILED COIL (POTENTIAL).
CONFLICT 233 233 L -> S (IN REF. 4).
SQ SEQUENCE 522 AA; 59143 MW; A0CF9574BCF6E974 CRC64;

Query Match 53.6%; Score 52; DB 1; Length 522;
Best Local Similarity 61.5%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
Db 117 GYGYGYGYGYG 129

RESULT 3
PTK AC100 STANDARD; PRT; 733 AA.
ID -PTK AC100
AC 052788;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase ptk (EC 2.7.1.112).
GN PTK.
OS Acinetobacter johnsonii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40214;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=98094281; PubMed=9434192;
RA Grangease C., Doublet P., Vaganay E., Vincent C., Deleage G.,
RA Duclos B., Cozzone A.J.;
RT "Characterization of a bacterial gene encoding an autophosphorylating
RT protein tyrosine kinase."
RL Gene 204:259-265(1997).
RN [2]
RN CHARACTERIZATION.
RP MEDLINE=96266486; PubMed=8683591;
RA Duclos B., Grangease C., Vaganay E., Riberty M., Cozzone A.J.;
RT "Autophosphorylation of a bacterial protein at tyrosine."
RL J. Mol. Biol. 259:891-895(1996).
RN [3]
RN MUTAGENESIS OF LYS-436; LYS-549; SER-550 AND ASP-651.
RP MEDLINE=99166918; PubMed=10069388;
RA Doublet P., Vincent C., Grangease C., Cozzone A.J., Duclos B.;
RT "On the binding of ATP to the autophosphorylating protein, Ptk, of the
RT bacterium Acinetobacter johnsonii."
RL FEBS Lett. 445:137-143(1999).
CC -1- FUNCTION: May be involved in the production and the transport of
CC exopolysaccharides.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- COFACTOR: Magnesium or manganese (Probable).
CC -1- PATHWAY: Exopolysaccharide biosynthesis.
CC -1- SUBCELLULAR LOCATION: Inner membrane.
CC -1- PTM: Autophosphorylated on several Tyr residues. Dephosphorylated
CC by pcp.
CC -1- SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
CC
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CC
CC EMBL; Y15162; CAA75431.1; -
CC ProSite; OS2789; -
CC InterPro; IPR003856; LPS_Wzz_MPA.
CC Pfam; PF02706; wzz; 1.
CC
CC Transferase; Tyrosine-protein kinase; Phosphorylation;
CC Exopolysaccharide synthesis; Transmembrane; Inner membrane;
CC ATP-binding; Magnesium; Manganese
CC TRANSMEM 19 39
CC TRANSMEM 438 458
CC NP_BIND 542 550
CC MUTAGEN 436 436 K->M: NO LOSS OF AUTOPHOSPHORYLATION.
CC MUTAGEN 549 549 K->M: LOSS OF AUTOPHOSPHORYLATION.
CC MUTAGEN 550 550 S->C: LOSS OF AUTOPHOSPHORYLATION.
CC MUTAGEN 651 651 D->N: LOSS OF AUTOPHOSPHORYLATION.
CC SEQUENCE 733 AA; 82362 MW; EF31482AF7B954 CRC64;
Query Match 53.6%; Score 52; DB 1; Length 733;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 GFGYSYNDYYX 12
DB 715 GYGYNAYAY 726

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RESULT 4
HEXA BLADI
ID HEXA BLADI STANDARD; PRT; 733 AA.
AC Q17127;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hexamerin precursor.
OS Hexamerin discoidalis (Tropical cockroach).
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Blaberus.
OX NCBI_TaxID=6981;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Fat body;
RA Jamroz R.C., Beintema J.J., Stam W.T., Bradfield J.Y.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Larval storage protein (LSP) which may serve as a store
CC of amino acids for synthesis of adult proteins (By similarity).
CC -1- SUBUNIT: Homohexamer (Potential).
CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U31328; AAA74579.1; -
CC HSP; P04253; LOXY
CC InterPro; IPR008922; Di-copper_centre.
CC InterPro; IPR008956; Hemocyanin_C.
CC InterPro; IPR005203; Hemocyanin_N.
CC InterPro; IPR005204; Hemocyanin_N.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00372; hemocyanin; 1.
CC Pfam; PF03723; hemocyanin_C; 1.
CC Pfam; PF03722; hemocyanin_N; 1.
CC PRINTS; PR00187; HAEMOCYANIN.
CC PROSITE; PS00209; HEMOCYANIN_1; FALSE_NEG.
CC PROSITE; PS00210; HEMOCYANIN_2; FALSE_NEG.
CC Signal; Storage protein; Glycoprotein.
CC SIGNAL 1 17
CC CHAIN 18 733
CC FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 234 234 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 431 431 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 733 AA; 87813 MW; 083DF739DD65729 CRC64;
Query Match 51.5%; Score 50; DB 1; Length 733;
Best Local Similarity 53.3%; Pred. No. 7.6;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 FGYSYNDYYGMDV 16
DB 345 YGYSTEHDYYYPEDL 359

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RESULT 5
CUTB LIMPO
ID CUTB LIMPO STANDARD; PRT; 59 AA.
AC P83360;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cuticle protein 7 isoform b (LpCp7b).
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;

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OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND PYRROLIDONE CARBOXYLIC ACID.
RC TISSUE=Carapace cuticle;
RA MEDLINE=22515710; PubMed=12628379;
RX Ditzel N., Andersen S.O., Hoejrup P.;
RT "Cuticular proteins from the horseshoe crab, Limulus polyphemus.";
RL Comp. Biochem. Physiol. 134B:489-497(2003).
CC -/- MASS SPECTROMETRY: MW=6970; METHOD=WALDI.
CC -/- SIMILARITY: Contains 1 cuticle consensus domain.
DR InterPro: IPR000618; Insect cuticle.
DR PROSITE: PS00233; CUTICLE; FALSE NEG.
KW Structural protein; Cuticle; PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT SEQUENCE 59 AA; 6987 MW; 9E05626F95A41B5 CRC64;
SQ
Query Match 50.5%; Score 49; DB 1; Length 59;
Best Local Similarity 61.5%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GFGYSYNYDYYG 13
Db 37 GFGKYPHYYPG 49

RESULT 6
HV2I HUMAN
ID HV2I HUMAN STANDARD; PRT; 146 AA.
AC P06331.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR: A02101; GIHFU2.
DR HSPG; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
FT SEQUENCE 146 AA; 16228 MW; 8D7FD52B8218171F CRC64;
SQ
Query Match 49.5%; Score 48; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 DYYGMDV 16
Db 128 DYYGMDV 135

RESULT 7
RALY MOUSE
ID RALY MOUSE STANDARD; PRT; 312 AA.
AC Q64012; Q99K76; Q9CXH8; Q9QZX6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA-binding protein Raly (hnRNP associated with lethal yellow protein)
DE (Maternally expressed hnRNP C-related protein).
GN RALY OR MERC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1); TISSUE SPECIFICITY, AND DEVELOPMENTAL
RP STAGE.
RC TISSUE=Embryo;
RX MEDLINE=93307655; PubMed=8319910;
RA Michaud E.J., Bultman S.J., Stubbs L.J., Woychik R.P.;
RT "The embryonic lethality of homozygous lethal yellow mice (Ay/ay) is
RT associated with the disruption of a novel RNA-binding protein.";
RL Genes Dev. 7:1203-1213(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RX MEDLINE=94326666; PubMed=8050375;
RA Dahl D.M., Stevens M.E., Vrieling H., Saxon P.J., Miller M.W.,
RA Epstein C.J., Barsh G.S.;
RT "Pleiotropic effects of the mouse lethal yellow (Ay) mutation
RT explained by deletion of a maternally expressed gene and the
RT simultaneous production of agouti fusion RNAs.";
RL Development 120:1695-1708(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RX STRAIN=C57BL/6J; TISSUE=Embryonic head;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fiehlmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1);
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Casavant T.L., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 100-135 FROM N.A. (ISOFORM 2).
RX MEDLINE=99431566; PubMed=10500250;
RA Khrebttukova I., Kuklin A., Woychik R.P., Michaud E.J.;
RT "Alternative processing of the human and mouse raly genes";
RL Biochim. Biophys. Acta 1447:107-112(1999).
CC -!- FUNCTION: Probable-RNA binding protein. Could be a heterogeneous
CC nuclear ribonucleoprotein (hnRNP).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=Q64012-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q64012-2; Sequence=VSP_005805;
CC -!- TISSUE SPECIFICITY: Widely expressed. Expressed in brain, testis,
CC lung, spleen and kidney. Weakly expressed in liver.
CC -!- DEVELOPMENTAL STAGE: Expressed in the unfertilized egg, in the
CC blastocyst, as well as in the developing embryo and fetus.
CC Expressed in developing skin.
CC -!- DISEASE: Defects in RALY are the cause of lethal yellow mutation
CC (A(y)), a dominant allele that cause embryonic lethality when
CC homozygous, and pleiotropic effects when heterozygous, including
CC yellow pelage, obesity, non-insulin dependent diabetes and
CC increased tumor susceptibility. A(y) is due to a 170 kb deletion
CC that removes all but the promoter and non-coding first exon of
CC RALY and links them to the ASIP/Agouti gene.
CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
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CC
CC EMBL; S72641; AAC60688.1; -;
CC EMBL; L17076; -; NOT ANNOTATED_CDS.
CC EMBL; AK014356; BAB29294.1; -;
CC EMBL; BC004851; AAH04851.1; -;
CC EMBL; BC016587; AAH16587.1; -;
CC EMBL; AF148458; AAF04488.1; -;
CC MGD; MGI:197850; Raly.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF00076; rrm; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC Ribonucleoprotein; RNA-binding; Nuclear protein; Alternative splicing.
FT DOMAIN 21 92
FT VARSPPLIC 110 125
FT Missing (in isoform 1).
FT /FTid=VSP_005805.
FT CONFLICT 249 249
FT G -> S (IN REF. 2 AND 3).
FT CONFLICT 281 281
FT T -> I (IN REF. 1).
SQ SEQUENCE 312 AA; 33158 MW; BF6BE0E8876BFC50 CRC64;

Query Match 49.58; Score 48; DB 1; Length 312;
Best Local Similarity 77.81; Pred. No. 6.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYSYNDYY 11
DB 111 GYSFDYDY 119

RESULT 8
OCLN_CANFA STANDARD; PRT; 521 AA.
AC Q28269;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Occludin.
GN OCLN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney; PubMed=8601611;
RA Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,
RA Itoh M., Yonemura S., Furuse M., Tsukita S.;
RT "Interspecies diversity of the occludin sequence: cDNA cloning of
RT human, mouse, dog, and rat-kangaroo homologues";
RL J. Cell Biol. 133:43-47(1996).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=97327764; PubMed=9182670;
RA Sakakibara A., Furuse M., Saitou M., Ando-Akatsuka Y., Tsukita S.;
RT "Possible involvement of phosphorylation of occludin in tight junction
RT formation.";
RL J. Cell Biol. 137:1393-1401(1997).
CC -!- FUNCTION: May play a role in the formation and regulation of the
CC tight junction (TJ) paracellular permeability barrier. Interacts
CC with ZO-1.
CC -!- SUBUNIT: Interacts with VAPA (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -!- DOMAIN: The C-terminal is cytoplasmic and is important for
CC interaction with ZO-1. Necessary for the tight junction
CC localization. Involved in the regulation of the permeability
CC barrier function of the tight junction (By similarity).
CC -!- PTM: PHOSPHORYLATED. LESS PHOSPHORYLATED FORMS ARE FOUND IN
CC BASOLATERAL MEMBRANE, CYTOSOL AND TIGHT JUNCTION. MORE HEAVILY
CC PHOSPHORYLATED FORMS ARE CONCENTRATED EXCLUSIVELY IN TIGHT
CC JUNCTION.
CC -!- SIMILARITY: Belongs to the ELL / occludin family.
CC
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CC
CC EMBL; U49221; AAC48582.1; -;
CC InterPro; IPR008253; Marvel.
CC InterPro; IPR002958; Occludin.
CC Pfam; PF01284; MARVEL; 1.
CC PRINTS; PR01258; OCLUDIN.
CC Tight junction; Transmembrane; Coiled coil; Phosphorylation.
KW DOMAIN 1 66
KW TRANSMEM 67 89
FT DOMAIN 90 134
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 135 159
FT TRANSMEM 160 169
FT DOMAIN 170 194
FT TRANSMEM 195 242
FT DOMAIN 243 264
FT TRANSMEM 265 521
FT DOMAIN 92 130
FT TYR/GLY-RICH.
FT DOMAIN 308 311
FT POLY-PRO.
FT DOMAIN 424 488
FT COILED COIL (POTENTIAL).

SQ SEQUENCE 521 AA; 59275 MW; 2875E59F8F0A1FFA CRC64;
 Query Match 49.5%; Score 48; DB 1; Length 521;
 Best Local Similarity 53.8%; Pred. No. 10;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYDYG 13
 Db 116 GYGFGYGYGYG 128

RESULT 9
 OCLN_CHICK STANDARD; PRT; 504 AA.
 AC Q91029;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Occludin.
 GN OCLN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRISUB=Embryonic brain;
 RX MEDLINE=94103332; Pubmed=8276896;
 RA Furuse M., Hirase T., Itoh M., Nagafuchi A., Yonemura S., Tsukita S.,
 RA Tsukita S.;
 RT "Occludin: a novel integral membrane protein localizing at tight
 RT junctions.";
 RL J. Cell Biol. 123:1777-1788(1993).
 CC -!- FUNCTION: May play a role in the formation and regulation of the
 CC tight junction (TJ) paracellular permeability barrier. Interacts
 CC with ZO-1.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells. Highly expressed in lung and
 CC liver. Expressed at a lower level in brain.
 CC -!- DOMAIN: The C-terminal is cytoplasmic and is important for
 CC interaction with ZO-1. Necessary for the tight junction
 CC localization. Involved in the regulation of the permeability
 CC barrier function of the tight junction. The second extracellular
 CC domain may also be implicated in the permeability barrier function
 CC of the tight junction.
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- SIMILARITY: Belongs to the ELL / occludin family.

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 EMBL; D21837; BA04865.1; -.
 PIR; A49467; A49467.
 InterPro; IPR008253; Marvel.
 Pfam; PF01284; MARVEL; 1.
 PRINTS; PR01258; OCLUDIN.
 Tight junction; Transmembrane; Coiled coil; Phosphorylation.
 FT DOMAIN 1 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 80 POTENTIAL.
 FT DOMAIN 81 123 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 124 148 POTENTIAL.
 FT DOMAIN 149 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 183 POTENTIAL.
 FT DOMAIN 184 227 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 228 249 POTENTIAL.

FT DOMAIN 250 504 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 82 119 TYR/GLY-RICH.
 FT DOMAIN 347 351 POLY-GLU.
 FT DOMAIN 363 370 POLY-ARG.
 FT DOMAIN 412 471 COILED COIL (POTENTIAL).
 SQ SEQUENCE 504 AA; 55863 MW; AD0352A45A0231FF CRC64;
 Query Match 48.5%; Score 47; DB 1; Length 504;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFGYSYNDYDYG 13
 Db 106 GLSYSYGYGYG 118

RESULT 10
 FRE4_YEAST STANDARD; PRT; 719 AA.
 AC P53746;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ferric reductase transmembrane component 4 precursor (EC 1.16.1.7)
 DE (Ferric-chelate reductase 4).
 DE FRE4 OR YNR060W OR N3518.
 GN Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duaterhose A., Floeth M., Fritz C., Heuss-Neitzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).
 CC -!- COPACITOR: FAD (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the FRE / CYBB family.

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 EMBL; Z71675; CA96342.1; -.
 PIR; S63392; S63392.
 GerMOnline; 143405; -.
 SGD; S0005343; FRE4.
 GO; GO:0005886; C:plasma membrane; IMP.
 GO; GO:0000293; F:ferric-chelate reductase activity; IMP.
 GO; GO:0015892; P:iron-siderochrome transport; IMP.
 InterPro; IPR002916; Ferric_reduct.
 Pfam; PF01794; Ferric_reduct; 1.
 Oxidoreductase; Electron transport; Transmembrane; Iron transport;
 KW FAD; NAD; Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 719 FERRIC REDUCTASE TRANSMEMBRANE COMPONENT
 FT NP_BIND 472 478 FAD (POTENTIAL).
 FT TRANSMEM 157 177 POTENTIAL.
 FT TRANSMEM 229 249 POTENTIAL.
 FT TRANSMEM 268 288 POTENTIAL.
 FT TRANSMEM 347 367 POTENTIAL.
 FT TRANSMEM 375 395 POTENTIAL.
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 647 647 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 696 696 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 719 719 9CA91F1F890AF1F9 CRC64;
SQ SEQUENCE 719 AA; 48.5%; Score 47; DB 1; Length 719;
Query Match 48.5%; Score 47; DB 1; Length 719;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 2 GYSYND--YYG 13
DB 147 YGYNNHDPYYFG 160

RESULT 11
YC81_METJA STANDARD; PRT; 1048 AA.
AC Q58677;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Hypothetical protein MJ1281.
GN MJ1281.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073 (1996).
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-----
DB EMBL; U67568; AAB99287.1; --
DR TIGR; MJ1281; --
KW Hypothetical protein; Complete proteome.
FT DOMAIN 598 601 POLY-GU.
SQ SEQUENCE 1048 AA; 121014 MW; 14138CFDCE6ABA76 CRC64;
Query Match 48.5%; Score 47; DB 1; Length 1048;
Best Local Similarity 72.7%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYSYNDYYG 13
DB 419 GYSYNEEYGG 429

RESULT 12
YK00_YEAST STANDARD; PRT; 201 AA.
ID YK00_YEAST
AC P36099;

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DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 23.0 kDa protein in YXR1-TPA1 intergenic region.
GN YKL030W OR YKL243.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-180 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94262309; PubMed=82031146;
RA Purnelle B., Skala J., van Dyck L., Goffeau A.;
RT "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new
RT tRNA gene and four new open reading frames including a leucine zipper
RT protein and a homologue to the yeast mitochondrial regulator ABF2."
RL Yeast 10:125-130 (1994).
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-----
DR EMBL; Z28029; CAA81864.1; --
DR EMBL; X71622; -; NOT_ANNOTATED_CDS.
DR PIR; S37847; S37847.
DR GEMOnline; 139786; --
DR SGD; S0001513; YKL030W.
KW Hypothetical protein.
SQ SEQUENCE 201 AA; 22956 MW; AF7B9798DFA88459 CRC64;
Query Match 47.4%; Score 46; DB 1; Length 201;
Best Local Similarity 72.7%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSYNDYYG 14
DB 25 YYYYYG 35

RESULT 13
ROR_HUMAN STANDARD; PRT; 633 AA.
AC O43390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein R (hnRNP R).
GN HNRPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98083170; PubMed=9421497;
RA Hassfeld W., Chan E.K.L., Mathison D.A., Portman D., Dreyfuss G.,
RA Steiner G., Tan E.M.;
RT "Molecular definition of heterogeneous nuclear ribonucleoprotein R
RT (hnRNP R) using autoimmune antibody: immunological relationship with
RT hnRNP P."
RL Nucleic Acids Res. 26:439-445 (1998).
CC -!- FUNCTION: Component of ribonucleosomes, which are complexes of at
CC least 20 other different heterogeneous nuclear ribonucleoproteins
CC (hnRNP). hnRNP play an important role in processing of precursor

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CC      mRNA in the nucleus.
CC      -!- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
CC      -!- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      -----
CC      EMBL: AF000364; AAC39540.1; -.
CC      PIR: T02673; T02673.
CC      HSP: P09651; IHA1.
CC      Genew: HGNC:5047; HNRPR.
CC      GK: C43390; -.
CC      MIM: 607201; -.
CC      GO: GO:0005634; C:nucleus; TAS.
CC      GO: GO:0008436; F:heterogeneous nuclear ribonucleoprotein; TAS.
CC      GO: GO:0003723; F:RNA binding; TAS.
CC      GO: GO:0006397; P:RNA processing; TAS.
CC      InterPro: IPR006535; hNRNP_R_Q.
CC      InterPro: IPR00504; hNRNP_R_Q.
CC      Pfam: PF00076; rrm; 3.
CC      SMART: SM00360; RRM; 3.
CC      TIGRFAMs: TIGR01648; hNRNP-R-Q; 1.
CC      PROSITE: PS00102; RRM; 3.
CC      PROSITE: PS00030; RRM_RNP; 1.
CC      Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.
CC      DOMAIN 1 153 ASP/GLU-RICH (ACIDIC).
CC      DOMAIN 412 418 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC      DOMAIN 165 244 RNA-BINDING (RRM) 1.
CC      DOMAIN 246 328 RNA-BINDING (RRM) 2.
CC      DOMAIN 341 411 RNA-BINDING (RRM) 3.
CC      DOMAIN 447 567 RNA-BINDING (RRM) 4.
CC      DOMAIN 462 497 G-Y-D-Y-H-D-Y.
CC      REPEAT 462 471 1 (APPROXIMATE).
CC      REPEAT 472 482 2 (APPROXIMATE).
CC      REPEAT 488 497 3 (APPROXIMATE).
CC      DOMAIN 579 633 GLN/ASN-RICH DOMAIN.
CC      SEQUENCE 633 AA; 70943 MW; 088341F6465ED46F CRC64;
CC
CC      Query Match 47.4%; Score 46; DB 1; Length 633;
CC      Best Local Similarity 57.1%; Pred. No. 25;
CC      Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CC
CC      QY      2 FGYSYNDYDYYGMD 15
CC      DB      465 YGEDYDYYGYD 478
CC
CC      RESULT 14
CC      NA95 HUMAN
CC      ID NA95 HUMAN STANDARD; PRT; 646 AA.
CC      AC Q9ULX6; Q94792; Q96J58; Q9NRQ0; Q9UGM0;
CC      DT 16-OCT-2001 (Rel. 40, Created)
CC      DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC      DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC      DE Neighbor of A-kinase anchoring protein 95 (Homologous to AKAP95
CC      DE protein) (HA95) (Helicase A-binding protein 95) (HAP95) (HRIHP2018).
CC      OS NAKAP95.
CC      GN Homo sapiens (Human).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC      OX NCBI_TaxID=9606;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RC TISSUE=Fetal brain;
CC      RX MEDLINE=20163068; PubMed=10697960;
CC      RA Seki N., Ueki N., Yano K., Saito T., Masuho Y., Muramatsu M.-A.;
CC      RT "CDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase

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RT      anchoring protein 95 (AKAP95) on chromosome 19p13.11-pl3.12 region.";
RL      J. Hum. Genet. 45:31-37(2000).
RP      SEQUENCE FROM N.A.
RX      MEDLINE=2022332; PubMed=10761695;
RA      Orstavik S., Eide T., Collas P., Han I.O., Tasken K., Kieff E.,
RA      Jansen I., Skalhogg B.S.;
RT      "Identification, cloning and characterization of a novel nuclear
RT      protein, HA95, homologous to A-kinase anchoring protein 95.";
RL      Biol. Cell 92:27-37(2000).
RP      SEQUENCE FROM N.A.
RX      TISSUE=Placenta and T-cell lymphoma;
RA      MEDLINE=20347256; PubMed=10748171;
RA      Westberg C., Yang J.-P., Tang H., Reddy T.R., Wong-Staal F.;
RT      "A novel shuttle protein binds to RNA helicase A and activates the
RT      retroviral constitutive transport element.";
RL      J. Biol. Chem. 275:21396-21401(2000).
RP      SEQUENCE FROM N.A.
RX      TISSUE=Placenta;
RA      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaby S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska J., Smalusz D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP      SEQUENCE OF 1-358 FROM N.A., AND SUBCELLULAR LOCATION.
RX      TISSUE=Fetal brain;
RA      MEDLINE=99068504; PubMed=9853615;
RA      Ueki N., Oda T., Kondo M., Yano K., Noguchi T., Muramatsu M.-A.;
RT      "Selection system for genes encoding nuclear-targeted proteins.";
RL      Nat. Biotechnol. 16:1338-1342(1998).
CC      -!- FUNCTION: Could play a role in constitutive transport element
CC      (CTE)-mediated gene expression. Does not seem to be implicated in
CC      the binding of regulatory subunit II of PKA.
CC      -!- SUBUNIT: Binds to the C-terminal of RNA helicase A.
CC      -!- SUBCELLULAR LOCATION: Nuclear at steady state but shuttles between
CC      the nucleus and cytoplasm.
CC
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      -----
CC      EMBL: AB025905; BAA5003.1; -.
CC      EMBL: AJ243467; CAB65092.1; -.
CC      EMBL: AF199414; AAF86048.1; -.
CC      EMBL: BC000713; AAF00713.1; -.
CC      EMBL: AB015332; BAA34791.1; ALT INIT.
CC      GO: GO:0005634; C:nucleus; TAS.
CC      GO: GO:0017151; F:DEAD/H-box RNA helicase binding; TAS.
CC      InterPro: IPR007071; AKAP95.
CC      InterPro: IPR007087; Znf_C2H2.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 42.6667 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ3

Perfect score: 97
Sequence: 1 gfgysynydyrgmdv 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	59.8	205	16 Q9A419	Q9A419 caulobacter
2	56	57.7	590	4 Q8TCC5	Q8TCC5 homo sapien
3	55	56.7	825	3 Q07834	Q07834 saccharomyc
4	52	53.6	152	5 Q86EL6	Q86EL6 schistosoma
5	52	53.6	779	16 Q8ABP9	Q8ABP9 bacteroides
6	52	53.6	3519	5 Q8IE65	Q8IE65 plasmodium
7	51	52.6	726	2 Q9RMD9	Q9RMD9 acinetobact
8	50	51.5	366	10 Q8SIT9	Q8SIT9 oryza sativ
9	50	51.5	753	5 Q8IIQ8	Q8IIQ8 plasmodium
10	50	51.5	770	17 Q8U3D2	Q8U3D2 pyrococcus
11	50	51.5	1089	16 Q8RE37	Q8RE37 fusobacteri
12	49.5	51.0	171	9 Q8SCT5	Q8SCT5 pseudomonas
13	49	50.5	1044	16 Q97GN9	Q97GN9 clostridium
14	49	50.5	1781	5 Q8ILK7	Q8ILK7 plasmodium
15	48	49.5	360	11 Q8CGB8	Q8CGB8 mus musculu
16	48	49.5	560	6 Q9N0W3	Q9N0W3 canis famil

17	48	49.5	560	13 Q802X5	Q802X5 brachydanio
18	48	49.5	785	11 Q8CBY3	Q8CBY3 mus musculu
19	48	49.5	795	4 Q8EPV6	Q8EPV6 homo sapien
20	48	49.5	800	4 Q8IZ27	Q8IZ27 homo sapien
21	48	49.5	812	16 Q8AA51	Q8AA51 bacteroides
22	48	49.5	1159	5 Q8IIN6	Q8IIN6 plasmodium
23	48	49.5	2900	5 Q8IEI2	Q8IEI2 plasmodium
24	47.5	49.0	105	16 Q9PLS4	Q9PLS4 chlamydia m
25	47	48.5	70	16 Q9KCN8	Q9KCN8 bacillus ha
26	47	48.5	126	11 Q8C3P0	Q8C3P0 mus musculu
27	47	48.5	142	5 Q9VC22	Q9VC22 drosophila
28	47	48.5	345	12 Q67G63	Q67G63 garlic late
29	47	48.5	1816	5 Q97275	Q97275 plasmodium
30	46.5	47.9	91	17 Q8TP77	Q8TP77 methanosarc
31	46	47.4	95	16 Q822E5	Q822E5 chlamydophi
32	46	47.4	101	16 Q8XWFS	Q8XWFS ralstonia s
33	46	47.4	132	16 Q8Y9W5	Q8Y9W5 listeria mo
34	46	47.4	210	16 Q9AAZ0	Q9AAZ0 caulobacter
35	46	47.4	243	4 Q7Z334	Q7Z334 homo sapien
36	46	47.4	307	11 Q8BL32	Q8BL32 mus musculu
37	46	47.4	483	17 Q980U1	Q980U1 sulfolobus
38	46	47.4	537	8 Q9B8W3	Q9B8W3 taenia cras
39	46	47.4	539	8 Q955Z6	Q955Z6 taenia soli
40	46	47.4	539	8 Q956A0	Q956A0 taenia soli
41	46	47.4	539	8 Q955Z5	Q955Z5 taenia soli
42	46	47.4	539	8 Q955Z9	Q955Z9 taenia soli
43	46	47.4	539	8 Q955Z7	Q955Z7 taenia soli
44	46	47.4	539	8 Q955Z8	Q955Z8 taenia soli
45	46	47.4	539	8 Q956A1	Q956A1 taenia soli

ALIGNMENTS

RESULT 1

Q9A419 PRELIMINARY; PRT; 205 AA.
AC Q9A419
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CC3024.
GN CC3024.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton R.J., Durkin A.S., Gwinn M.L., Hatt D.H.,
RA DeBoy R.T., Dodson R.J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Kolonay J.F., Smit J., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus";
PRC. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL EMBL; AE005965; AA024986.1; -.
DR PIR; F87623; F87623.
DR TIGR; CC3024; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 205 AA; 22665 MW; C03B0E4FC08908E8 CRC64;

Query Match 59.8%; Score 58; DB 16; Length 205;

Best Local Similarity 58.8%; Pred. No. 1.3;

Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 GFGYSYNDY----YIG 13

DB 165 GYGCDYDYAPRYG 181

QY 1 GCGSYNDYDY 12
Db 795 GYGTYDYDY 806

RESULT 4
Q86EL6 PRELIMINARY; PRT; 152 AA.
AC Q86EL6
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Clone ZD208 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu F., Hu W., Yan Q., Xu X., Zhu Z., Zhang X., Wang J., Sun J.,
RA Xu X., Wang Z., Zeng L., Rong Y., Wu X., Qu J., Xu Z., Huang J.,
RA Ma Y., Wang S., Wang Z., Xue C., Feng Z., Chen Z., Han Z.,
PT "The full-length cDNA of S. japonicum genes";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY223200; AAP06321.1;
SQ SEQUENCE 152 AA; 17239 MW; FC68629092B0E878 CRC64;

Query Match 53.6%; Score 52; DB 5; Length 152;
Best Local Similarity 61.5%; Pred. No. 6.9;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 YSYNDYDYGM 16
Db 126 YSYHHQYDYD 138

RESULT 5
Q8ABP9 PRELIMINARY; PRT; 779 AA.
AC Q8ABP9
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative tyrosine-protein kinase ptk.
GN BT0061.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.,
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076 (2003).
DR EMBL; AF016926; AAO75168.1;
DR GO; GO:0002793; C:external outer membrane (sensu Gram-negativ. .; IEA.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008952; P:defense response; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR InterPro; IPR001800; Lipoprotein_6.
DR InterPro; IPR003856; LPS_Wzz_MPA.
DR Pfam; PF02706; wzz; 1.
DR ProDom; PD001149; Lipoprotein_6; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 779 AA; 87242 MW; FF30209278D8P430 CRC64;

Query Match 53.6%; Score 52; DB 16; Length 779;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGSYNDYDY 12
Db 795 GYGTYDYDY 806

RESULT 2
Q8TCC5 PRELIMINARY; PRT; 590 AA.
AC Q8TCC5
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022389; AAH22389.1;
DR GO; GO:0003484; F:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase; 1.
DR PROSITE; PS00523; SULFATASE_1; 1.
DR PROSITE; PS00149; SULFATASE_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 590 AA; 65965 MW; F02B6823B40AE78B CRC64;

Query Match 57.7%; Score 56; DB 4; Length 590;
Best Local Similarity 72.7%; Pred. No. 7.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSYNDYDYGM 14
Db 155 YNYGFDYDYGM 165

RESULT 3
Q07834 PRELIMINARY; PRT; 825 AA.
AC Q07834
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Chromosome XII reading frame ORF YLL032C.
GN YLL032C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dueterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mifs;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KH DOMAIN.
DR EMBL; Z73137; CAA97481.1;
DR PIR; S64783; S64783.
DR SGD; S0003955; YLL032C.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004087; KH_dom.
DR Pfam; PF00013; KH; 1.
DR SMART; SM00322; KH; 1.
SQ SEQUENCE 825 AA; 94596 MW; 00ADD65FBF1FA9FA CRC64;

Query Match 56.7%; Score 55; DB 3; Length 825;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
 :|||:|
 Db 757 GYGYGYGYG 769

RESULT 6
 Q8IE65 PRELIMINARY; PRT; 3519 AA.
 AC Q8IE65;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical malaria antigen.
 GN M26-32-10.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
 RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
 RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrall B.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL844509; CAD52401.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 3519 AA; 419077 MW; 15C47FF2C08C5393 CRC64;

Query Match 53.6%; Score 52; DB 5; Length 3519;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMD 15
 :|||:|
 Db 1027 GKGYNYNYNDDDD 1041

RESULT 7
 Q9RMD9 PRELIMINARY; PRT; 726 AA.
 AC Q9RMD9;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Protein tyrosine kinase.
 GN WZC.
 OS Acinetobacter lwoffii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=28090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakar D., Gutnick D.L.;
 RC STRAIN=RAG-1;
 RT "Genomic organization of the wce region of Acinetobacter lwoffii RAG-1
 RT required for emulsan biosynthesis."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RAG-1;
 RA Nakar D., Gutnick D.L.;
 RT "A protein tyrosine kinase of Acinetobacter lwoffii RAG-1 is involved
 RT in emulsan biosynthesis."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243431; CAB57193.1; -
 DR PIR; T44825; T44825.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0009103; F:kinase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR InterPro; IPR003856; IFS_Wzz_MPA.
 DR Pfam; PF02706; wzz; 1.
 KW Kinase.
 SQ SEQUENCE 726 AA; 81609 MW; 845BDEDD73E09C0E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 726;
 Best Local Similarity 75.0%; Pred. No. 50;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 12
 :|||:|
 Db 709 GAGYSYNAYAY 720

RESULT 8
 Q8S1T9 PRELIMINARY; PRT; 386 AA.
 AC Q8S1T9;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE P0506B12.3 protein (P0460C04.23 protein).
 GN P0506B12.3 OR P0460C04.23.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone.P0506B12."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone.P0460C04."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003271; BAB89731.1; -
 DR EMBL; AP004366; BAB92930.1; -
 DR Gramene; Q8S1T9; -
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR004314; DUF239.
 DR Pfam; PF03080; DUF239; 1.
 SQ SEQUENCE 386 AA; 42354 MW; DD4AED7939404EFD CRC64;

Query Match 51.5%; Score 50; DB 10; Length 386;
 Best Local Similarity 57.1%; Pred. No. 36;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GYSYNDYYGMDV 16
 :|||:|
 Db 66 GYEMNSQYYGIEV 79

RESULT 9
 Q8I1Q8 PRELIMINARY; PRT; 753 AA.
 AC Q8I1Q8;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN PF00845W.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Muncall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

RESULT 13


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Q97GN9          PRELIMINARY;          PRT; 1044 AA.
ID AC Q97GN9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glycosyltransferase domain containing protein.
GN CAC327.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AB007733; AAK80283.1; -.
DR PIR; H97186; H97186.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR InterPro; IPR001173; Glyco_transf_2.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Transferrase; Complete proteome.
SQ SEQUENCE 1044 AA; 121349 MW; C1F2F7E651C39F2 CRC64;

Query Match 50.5%; Score 49; DB 16; Length 1044;
Best Local Similarity 64.3%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 GYSYNYDYDYGYGMDV 16
DB 143 GYGYQYD--YGMDI 154
||| ||| ||| |||
||| ||| ||| |||

RESULT 14
Q8ILK7          PRELIMINARY;          PRT; 1781 AA.
ID AC Q8ILK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN PF14_0236.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.M.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Aguioli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McPadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014819; AAN36849.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.

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DR InterPro; IPR000571; Znf_CCH.
DR Pfam; PF00642; zf-CCH; 2.
DR SMART; SM00356; Znf_C3H1; 2.
KW Hypothetical protein.
SQ SEQUENCE 1781 AA; 211749 MW; E4E19022A14C46F0 CRC64;

Query Match 50.5%; Score 49; DB 5; Length 1781;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 FGYSYNYDYGYGMDV 15
DB 1114 YNYNYNYNYAYD 1127
||| ||| ||| |||
||| ||| ||| |||

RESULT 15
Q8CGB8          PRELIMINARY;          PRT; 360 AA.
ID AC Q8CGB8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to hypothetical protein 9330175N02.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041775; AAH41775.1; -.
KW Hypothetical protein.
SQ SEQUENCE 360 AA; 39183 MW; DA00242A347C7709 CRC64;

Query Match 49.5%; Score 48; DB 11; Length 360;
Best Local Similarity 46.7%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 FGYSYNYDYGYGMDV 16
DB 94 YNYAYPYSYYPMSM 108
||| ||| ||| |||
||| ||| ||| |||

Search completed: April 21, 2004, 17:37:16
Job time : 44.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 32.9099 Seconds
(without alignments)
1035.433 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLISLSPGERAT.....CQVGSPPCSFGQTKLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organalle.*
9: sp_phages.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	92.8	109	4 Q9UL78	Q9ul78 homo sapien
2	504	90.3	109	4 Q9UL86	Q9ul86 homo sapien
3	435.5	78.0	108	4 Q9UL83	Q9ul83 homo sapien
4	426	76.3	109	4 Q9UL85	Q9ul85 homo sapien
5	398.5	71.4	108	4 Q9UL79	Q9ul79 homo sapien
6	390.5	70.0	108	4 Q9UL77	Q9ul77 homo sapien
7	386.5	69.3	108	4 Q9UL70	Q9ul70 homo sapien
8	384	68.8	114	11 Q8K1F1	Q8klf1 mus musculu
9	383.5	68.7	131	11 Q8L1C3	Q8llc3 mus musculu
10	382.5	68.5	236	4 Q7Z3Y4	Q7z3y4 homo sapien
11	381	68.3	107	4 Q96SA9	Q96sa9 homo sapien
12	378.5	67.8	234	4 Q7Z473	Q7z473 homo sapien
13	364.5	65.3	237	13 Q7SZ36	Q7sz36 xenopus lae
14	364	65.2	239	4 Q8NEK0	Q8nek0 homo sapien
15	362	64.9	107	4 Q9UL81	Q9ul81 homo sapien
16	362	64.9	112	11 Q8K1F2	Q8klf2 mus musculu

17	361	64.7	112	11 Q8K1E3	Q8klf3 mus musculu
18	358.5	64.2	111	11 Q920E9	Q920e9 mus musculu
19	358	64.2	106	5 Q9U410	Q9u410 schistosoma
20	356.5	63.9	111	11 Q8L1U6	Q8llue mus musculu
21	355	63.6	238	11 Q99M37	Q99m37 mus musculu
22	347	62.2	238	11 Q8VCI6	Q8vci6 mus musculu
23	345.5	61.9	107	11 Q9ERZ9	Q9erz9 mus musculu
24	343.5	61.6	234	11 Q8R062	Q8r062 mus musculu
25	343	61.5	134	11 Q8VDD0	Q8vdd0 mus musculu
26	341.5	61.2	236	11 Q7TMK3	Q7tmk3 mus musculu
27	341	61.1	239	4 Q8TCD0	Q8tcd0 homo sapien
28	340	60.9	239	11 Q8VC55	Q8vc55 mus musculu
29	339.5	60.8	108	11 Q8VIJ0	Q8vij0 mus musculu
30	338.5	60.7	99	11 Q9JL74	Q9jl74 mus musculu
31	338	60.6	235	11 Q9LW12	Q9lws12 mus musculu
32	337.5	60.5	233	11 Q9LWS9	Q9lws9 mus musculu
33	334.5	59.9	109	11 Q920E6	Q920e6 mus musculu
34	334.5	59.9	214	11 Q9RIAS	Q9rias mus musculu
35	334	59.9	112	11 Q8K1F0	Q8klf0 mus musculu
36	333.5	59.8	116	4 Q96PF6	Q96pf6 homo sapien
37	333.5	59.8	234	11 Q8VCP0	Q8vcp0 mus musculu
38	333.5	59.8	298	11 Q9QYF0	Q9qyf0 mus musculu
39	333	59.7	235	11 Q7TMK0	Q7tmk0 mus musculu
40	331.5	59.4	101	11 Q9JL78	Q9jl78 mus musculu
41	329.5	59.1	114	4 Q9UL80	Q9ul80 homo sapien
42	329.5	59.1	236	11 Q7TS98	Q7ts98 mus musculu
43	328.5	58.9	234	11 Q9LWF8	Q9lwf8 mus musculu
44	323	57.9	104	11 Q9JL82	Q9jl82 mus musculu
45	322.5	57.8	107	11 Q9JL84	Q9jl84 mus musculu

ALIGNMENTS

RESULT 1
Q9UL78 PRELIMINARY; PRT; 109 AA.
ID Q9UL78
AC Q9UL78; 2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Marwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; --
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.

DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

Query Match 92.8%; Score 518; DB 4; Length 109;
Best Local Similarity 93.5%; Pred. No. 3.2e-49;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDCAVYCCQYGGSPFLTFGGTKVEIK 108

RESULT 2
QYUL86 PRELIMINARY; PRT; 109 AA.
AC QYUL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 90.3%; Score 504; DB 4; Length 109;
Best Local Similarity 91.7%; Pred. No. 1.1e-47;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFLTFGGTKVDIK 108

RESULT 3
QYUL83 PRELIMINARY; PRT; 108 AA.
AC QYUL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 78.0%; Score 435.5; DB 4; Length 108;
Best Local Similarity 79.6%; Pred. No. 3.7e-40;
Matches 86; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLLIYATSSRATGIP 59

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
DB 60 ARFGSGSGTDFLTISRLEPEDFAVYCCQYHNNWFFTFGGTKVDIK 107

RESULT 4
QYUL85 PRELIMINARY; PRT; 109 AA.
AC QYUL85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR PIR; B30609; D30609.

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DR HSSP; P80362; LWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; F81E43E7C7AFAPACC CRC64;

Query Match 76.3%; Score 426; DB 4; Length 109;
Best Local Similarity 78.0%; Pred. No. 4.2e-39;
Matches 85; Conservative 11; Mismatches 11; Indels 2; Gaps 2;

Qy 1 EIVLTQSPGTLSPGERATLSCASQSVSSYLAWYQQKPKGAPRLIIYATSSRATGIP 60
Db 1 EIVMTQSPATLSVSPGERATLSCWASQSISSN-LAWYQQKPKGAPRLIIYATSSRATGIP 59

Qy 61 DRFGSGSGTDFTLTISRLPEDFAVYYCQQYSGSPSCFGQTKLEIK 108
Db 60 ARFSGSGGTFTLTISLQSEDFAIHCQQYNWPLTFGGTKVEIK 108

RESULT 5
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CD16F3 CRC64;

Query Match 70.0%; Score 390.5; DB 4; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.3e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCASQSVSSYLAWYQQKPKGAPRLIIYATSSRATGIP 60
Db 1 DIQMTQSPSLASGVDRVTITCRASQSI-SYLLAWYQQKPKAPRLIIYATSSRATGIP 59

Qy 61 DRFGSGSGTDFTLTISRLPEDFAVYYCQQYSGSPSCFGQTKLEIK 108
Db 60 SRFGSGSGTDFTLTISLQSEDFATYYCQQSYSTWTFEGTKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; P0863; P0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724PB4E CRC64;

Query Match 71.4%; Score 398.5; DB 4; Length 108;
Best Local Similarity 71.3%; Pred. No. 4.3e-36;
Matches 77; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCASQSVSSYLAWYQQKPKGAPRLIIYATSSRATGIP 60
Db 1 DIQMTQSPSLASGVDRVTITCRMSQGI-SYLLAWYQQKPKAPRLIIYATSSRATGIP 59

Qy 61 DRFGSGSGTDFTLTISRLPEDFAVYYCQQYSGSPSCFGQTKLEIK 108
Db 60 SRFGSGSGTDFTLTISLQSEDFATYYCQQYSPPTTFGGTKVEIK 107

RESULT 6
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CD16F3 CRC64;

Query Match 70.0%; Score 390.5; DB 4; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.3e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCASQSVSSYLAWYQQKPKGAPRLIIYATSSRATGIP 60
Db 1 DIQMTQSPSLASGVDRVTITCRASQSI-SYLLAWYQQKPKAPRLIIYATSSRATGIP 59

Qy 61 DRFGSGSGTDFTLTISRLPEDFAVYYCQQYSGSPSCFGQTKLEIK 108
Db 60 SRFGSGSGTDFTLTISLQSEDFATYYCQQSYSTWTFEGTKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; P0863; P0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724PB4E CRC64;

Query Match 71.4%; Score 398.5; DB 4; Length 108;
Best Local Similarity 71.3%; Pred. No. 4.3e-36;
Matches 77; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCASQSVSSYLAWYQQKPKGAPRLIIYATSSRATGIP 60
Db 1 DIQMTQSPSLASGVDRVTITCRMSQGI-SYLLAWYQQKPKAPRLIIYATSSRATGIP 59

Qy 61 DRFGSGSGTDFTLTISRLPEDFAVYYCQQYSGSPSCFGQTKLEIK 108
Db 60 SRFGSGSGTDFTLTISLQSEDFATYYCQQYSPPTTFGGTKVEIK 107

RESULT 6
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;

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FT NON TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 69.3%; Score 386.5; DB 4; Length 108;
Best Local Similarity 66.7%; Pred. No. 9.1e-35;
Matches 72; Conservative 17; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
Db 1 DIQWTSFSSLSASVGDVTTTCRASQGI-SNYLAWYQQKPGKPKVPSKLIYAASLTQSGVP 59

QY 61 DRFSGSGGTDFTLTISLRLEPEDFPAVYCCQYGGSPCSFGGQTKLEIK 108
Db 60 SRFGSGSGGTDFTLTISLSQEDVATYCCQKNSAPRTFPGGQTKLEIK 107

RESULT 8
Q8K1F1 PRELIMINARY; PRT; 114 AA.
AC Q8K1F1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Teguchi H., Plaque S., Karle S., Nishiyama Y., Paul S.;
RT "Immune proteolytic antibodies: Failed D-vipase response to the D-
entantioner of VIP and identification of L-vipase Vi domains.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516284; AAM64202.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match 68.8%; Score 384; DB 11; Length 114;
Best Local Similarity 67.6%; Pred. No. 1.9e-34;
Matches 73; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
Db 1 DIVLTQSPALMSASPGKVTMTCRASSVSSVYLHWYQQKSGSPKLIWYSTNLSAGVP 60

QY 61 DRFSGSGGTDFTLTISLRLEPEDFPAVYCCQYGGSPCSFGGQTKLEIK 108
Db 61 ARFSGSGGTDFTLTISLRLEPEDFPAVYCCQYGGSPCSFGGQTKLEIK 108

RESULT 9
Q811C3 PRELIMINARY; PRT; 131 AA.
AC Q811C3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MRL/MPJ-1pr/1pr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833;
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephritogenic monoclonal
antibodies derived from an MRL/lpr lupus mouse.";
RL Mol. Immunol. 30:177-182(1993).
DR EMBL; D14629; BAA03482.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 >131 IMMUNOGLOBULIN GAMMA-3 KAPPA CHAIN.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14083 MW; 5E8365695466E9E CRC64;

Query Match 68.7%; Score 383.5; DB 11; Length 131;
Best Local Similarity 67.0%; Pred. No. 2.5e-34;
Matches 73; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
Db 23 QIVLTQSPALMSASPGKVTMTCRASSVSSVYLHWYQQKSGSPKLIWYSTNLSAGVP 82

QY 61 DRFSGSGGTDFTLTISLRLEPEDFPAVYCCQYGGSP-CSFGGQTKLEIK 108
Db 83 VRFGSGSGGTDFTLTISLRLEPEDFPAVYCCQYGGSPCSFGGQTKLEIK 131

RESULT 10
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny K.C., Hulse S., Garcia A.M., Gay L.J., Hulyk S.W.,
Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Schmutz J., Schmechel J.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Schmechel J.E.,
Krzyszynski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA05332.1; -
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 68.5%; Score 382.5; DB 4; Length 236;
Best Local Similarity 66.7%; Pred. No. 6.7e-34;
Matches 72; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQQKPGQAPRLLIYATSSRATGIP 60
Db 23 DIQMTQSPSSLSASVGTVTITCRASQDI-SNYLAWFOQKPGKAPKSLIYGASSLQSGVQ 81

QY 61 DRPSGSGSGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108
Db 82 SKFSGSGSGTDFTLTISRLEPEDFAVYCCQYKSVPTFGGTKLEIK 129

RESULT 11
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.B., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AA868785.1; -
DR EIR; B49047; B49047.
DR EIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9CB577F16 CRC64;

Query Match 68.3%; Score 381; DB 4; Length 107;
Best Local Similarity 69.4%; Pred. No. 3.6e-34;
Matches 75; Conservative 14; Mismatches 17; Indels 2; Gaps 2;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQQKPGQAPRLLIYATSSRATGIP 60
Db 1 DIQMTQSPSSLSASVGTVTITCRASQSI-SSYLNWYQKPGKAPKLLIYAASLQSGVP 59

QY 61 DRPSGSGSGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108
Db 60 SRFSGSGSGTDFTLTISRLEPEDFAVYCCQYKSVPTFGGTKLEIK 106

RESULT 12
Q7Z473 PRELIMINARY; PRT; 234 AA.
ID Q7Z473
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Joquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98375893; PubMed=9712075;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AA856256.1; -
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 67.8%; Score 378.5; DB 4; Length 234;
Best Local Similarity 67.3%; Pred. No. 1.8e-33;
Matches 72; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

QY 2 IVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQQKPGQAPRLLIYATSSRATGIP 61
Db 22 IRMTQSPSSASGTDRVTITCRASQSI-GSYLAWYQKPGKAPQLLIYAASLQSGVPS 80

QY 62 RFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108
Db 81 RFSGSGSGTDFTLTISRLEPEDFAVYCCQYKSVPTFGGTKLEIK 127

RESULT 13
Q7SZ36 PRELIMINARY; PRT; 237 AA.
ID Q7SZ36
AC Q7SZ36;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22344132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";

Search completed: April 21, 2004, 17:03:47
Job time : 33.9099 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:55:26 ; Search time 47.279 Seconds
        (without alignments)
        645.427 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQPGTSLSPGERAT.....CQYGSPPCSFGQTKLEIK 108

Scoring table: BLOSUM62
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Searched: 1586107 seqs, 282547505 residues

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RESULT 1
AAR38672
ID AAR38672 standard: protein: 129 AA.

ID
 XX
 AC

XX
DT 25-MAR-2003 (revised)

DT 01-NOV-1993 (first entry)
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DE vk325-Jk2.
XX

Monoclonal antibody; MAb; envelope; receptor; hybridoma; polymerase chain reaction; immune deficiency

epitope; immune deficiency.

OS	HOME	NAME
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FT Peptide 1.20
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FT Misc-difference 1
FT /note= "Met encoded
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FT	Region	71	77

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FT      /note= "Leu encoded
FT      110. .117
FT      Region

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FT /label= CDR3
FT Misc-difference 113

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FT	/note= "Gly encoded
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FT      /note= "Ser encoded
FT      Misc-difference 116

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FT	Region	/note= "pro encoded
FT		117. .129
FT		/label= 1k3

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FN NO9512232-AT.
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PD 24-JUN-1993.

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SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	535	95.9	129	2	AAR38672	Aar38672 vk325-Jk2
2	533	95.5	130	6	ABJ36930	Ant1-CD40
3	533	95.5	384	4	AM24101	Human EST
4	532	95.3	120	7	ADD40551	3E1/4G11
5	530	95.0	384	4	AAU14462	Human nov
6	530	95.0	384	4	AAU14463	Human nov
7	530	95.0	384	4	AAU14461	Human nov
8	530	95.0	384	4	AAU14464	Human nov
9	526	94.3	108	6	AAE38059	Human 17G
10	526	94.3	109	6	ADA89268	Human ant
11	525.5	94.2	131	6	ABP57366	Anti-T-TRA1
12	524.5	94.0	109	5	ABG32514	Human VK
13	524.5	94.0	226	4	ABP99397	Human int
14	524.5	94.0	226	4	ABP99374	Human int
15	524.5	94.0	226	4	ABP5007	Anti-IL8
16	524.5	94.0	226	4	ABP75030	Anti-IL8
17	524	93.9	109	6	AAE35209	Human IGE
18	522.5	93.6	109	2	AAW84096	Human V k
19	522	93.5	109	6	ADA89220	Human ant
20	522	93.5	131	5	ABP62199	Human imm
21	522	93.5	134	5	ABP62186	Human imm
22	521.5	93.5	109	5	ABP62186	Human imm
23	521.5	93.5	109	5	ABP62200	Human imm
24	521	93.4	134	5	ABP62200	Human imm
25	521	93.4	134	5	ABP62210	Human imm


```

XX PF 10-DEC-1992; 92WO-US010928.
XX PR 10-DEC-1991; 91US-00804652.
XX (DAND ) DANA FARBER CANCER INST INC.
XX PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
XX PI Marasco WA, Sodroski JG, Posner MR, Haseitine WA;
XX WPI; 1993-214174/26.
XX DR N-PSDB; AAQ42706.
XX DNA segments encoding monoclonal antibody - which binds to gp120 and
XX neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV
XX infection.
XX Disclosure; Page 74-75; 109pp; English.
XX The nucleotide sequence of F105 V $\kappa$  (AAQ42707 - sequence differs from
XX other F105 V $\kappa$  sequences given elsewhere in the specification) was
XX compared with germline gene HumvX325 (AAQ42706), showing 97.7%
XX similarity. By nucleotide sequence analysis, F105 appears to be derived
XX from a member of the V $\kappa$  III subgroup gene family. (Updated on 25-MAR-2003
XX to correct PN field.)
XX Sequence 129 AA;
SQ
Query Match 95.9%; Score 535; DB 2; Length 129;
Best Local Similarity 96.3%; Pred. No. 1.8e-33;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFGSGSGTDTLTISRLEPEDFAVYQCQYGGSPFCFGQGTKLEIK 108
DB 81 DRFGSGSGTDTLTISRLEPEDFAVYQCQYGGSPYTFGQGTKLEIK 128
RESULT 2
ABJ36930
ID ABJ36930 standard; protein; 130 AA.
AC ABJ36930;
XX
XX 01-MAY-2003 (first entry)
XX Anti-CD40 monoclonal antibody related protein SEQ ID No 46.
XX Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
XX human CD40; IL-12; LPS; lipopolysaccharide; IFN $\gamma$ ; interferon gamma;
XX dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
XX immunosuppressor; anti-tumour agent; immunosuppressant; allergy;
XX autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.
XX Unidentified.
XX WO200288186-A1.
XX
XX 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-JP004292.
XX
XX 27-APR-2001; 2001WO-US013672.
XX 11-MAY-2001; 2001JP-00142482.
XX 05-OCT-2001; 2001JP-00310535.
XX 26-OCT-2001; 2001US-00040244.
XX (KIRI ) KIRIN BEER KK.
XX
XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;
PI

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XX WPI; 2003-120463/11.
XX DR N-PSDB; ABT31872.
XX
XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
XX or functional fragment, is useful in the treatment of e.g. autoimmune
XX diseases or cancer.
XX
XX Claim 25; Page 51; 94pp; Japanese.
XX
XX The invention relates to an antibody to human CD40, or its functional
XX fragment, has at least one of the following properties: acting on
XX dendritic cells to produce IL-12 in the presence of LPS
XX (lipopolysaccharide) and IFN $\gamma$  (interferon gamma); acting on dendritic
XX cells to activate maturation of the dendritic cells with high G28-5
XX antibody; and activating CD95 expression with high G28-5 antibody against
XX B cell line. Such antibodies or functional fragments can be used as
XX immunosuppressors, anti-tumour agents, immunosuppressants, and as remedies
XX for autoimmune diseases, allergy or coagulation factor VIII inhibitors
XX syndrome. This sequence represents a protein relating to the anti-CD40
XX monoclonal antibody of the invention
XX
XX Sequence 130 AA;
SQ
Query Match 95.5%; Score 533; DB 6; Length 130;
Best Local Similarity 95.4%; Pred. No. 2.5e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFGSGSGTDTLTISRLEPEDFAVYQCQYGGSPFCFGQGTKLEIK 108
DB 81 DRFGSGSGTDTLTISRLEPEDFAVYQCQYGGSPYTFGQGTKLEIK 128
RESULT 3
AAM24101
ID AAM24101 standard; protein; 384 AA.
XX
XX AAM24101;
XX
XX 12-OCT-2001 (first entry)
XX Human EST encoded protein SEQ ID NO: 1626.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
XX gene therapy; nutrition.
XX
XX Homo sapiens.
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US002687.
XX
XX 25-JAN-2000; 2000US-00491404.
XX 17-JUL-2000; 2000US-00617746.
XX 03-AUG-2000; 2000US-00631451.
XX 15-SEP-2000; 2000US-00663870.
XX
XX (HYSB-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
XX DR N-PSDB; AAH98760.
XX

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PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS
XX Claim 20; Page 1102-1103; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
XX Sequence 384 AA;
SQ
Query Match 95.5%; Score 533; DB 4; Length 384;
Best Local Similarity 95.4%; Pred. No. 6.9e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 167 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 226
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 108
DB 227 DRFSGSGGTDFLTISRLEPEDFAVYCCQYVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 274
RESULT 4
ADD40551
ID ADD40551 standard; protein; 120 AA.
XX
AC ADD40551;
XX
DT 15-JAN-2004 (first entry)
DE 3E1/4G11 light chain variable region.
XX
KW Human; human Fas ligand; hFasL; antibody;
KW systemic inflammatory response syndrome; sepsis;
KW multiple organ dysfunction syndrome; acute respiratory distress syndrome;
KW trauma; graft-versus-host disease; organ rejection; multiple sclerosis;
KW idiopathic pulmonary fibrosis; osteoarthritis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW acute myocardial infarction; cardiomyopathy; cardiac reperfusion injury;
KW diabetes; cancer; HIV infection; influenza virus; hepatic disorder;
KW renal disorder; anti-infective; antibacterial; cardiac; osteopathic;
KW virucide; anti-HIV; cytostatic; antidiabetic; nephrotropic; hepatotropic;
KW immunosuppressive; vulnary; gene therapy; vaccine;
KW light chain variable region; 3E1; 4G11.
XX
OS Homo sapiens.
XX
XX WO2003079750-A2.
XX
XX 02-OCT-2003.
XX
XX 12-MAR-2003; 2003WO-US006155.
XX
XX 21-MAR-2002; 2002US-0367054P.
XX
XX 10-SEP-2002; 2002US-0409768P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Lancaster JS;
XX
XX WPI; 2003-876866/81.
XX
XX N-PSDB; ADD40550.
XX
XX New isolated anti-hFasL human antibody or its antigen-binding portion,
PT useful for preparing a composition for neutralizing hFasL activity for
PT treating or preventing a disorder in which hFasL activity is detrimental,

PT e.g. sepsis.
XX
PS Claim 1; SEQ ID NO 2; 55pp; English.
XX
CC The present invention relates to anti-human Fas ligand (hFasL) antibodies
CC or their antigen-binding portion (I). (I) are useful for preparing a
CC composition for neutralizing FasL activity for treating or preventing a
CC disorder in which FasL activity is detrimental, e.g. systemic
CC inflammatory response syndrome, sepsis, multiple organ dysfunction
CC syndrome, acute respiratory distress syndrome, trauma, graft-versus-host
CC disease, organ rejection associated with organ transplant, multiple
CC sclerosis, idiopathic pulmonary fibrosis, osteoarthritis, inflammatory
CC bowel disease, Crohn's disease, ulcerative colitis, acute myocardial
CC infarction, cardiomyopathy, cardiac reperfusion injury, diabetes, cancer,
CC HIV infection, influenza virus infection, hepatic disorders including but
CC not limited to fulminant viral hepatitis B or C, chronic hepatitis C
CC virus, chronic hepatitis B virus, alcoholic hepatitis, hepatic cirrhosis
CC or renal disorders. The present sequence is a light chain variable region
CC (LCVR) of anti-FasL antibodies 3E1 or 4G11.
XX
XX Sequence 120 AA;
SQ
Query Match 95.3%; Score 532; DB 7; Length 120;
Best Local Similarity 95.4%; Pred. No. 2.8e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 108
RESULT 5
AAU14462
ID AAU14462 standard; protein; 384 AA.
XX
AC AAU14462;
XX
DT 24-OCT-2001 (first entry)
DE Human novel protein #333.
XX
KW Human; novel protein; Anianaemic; osteopathic; anti-inflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
XX WO200155437-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US002623.
XX
XX 25-JAN-2000; 2000US-00491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22767.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
PT

PS Example 4; Page 825-826; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or
 CC their active domains. The polypeptides, polynucleotides and antibodies
 CC raised against the polypeptides are used in a method of treatment of a
 CC mammal and prevention of disorders caused by the aberrant protein
 CC expression or activity. The polypeptides can be used as molecular weight
 CC markers, food supplements, and in antibody production. The polypeptides
 CC are used to identify compounds which bind to the polypeptides.
 CC Polynucleotides of the invention are used as probes and primers, for
 CC sequencing, for chromosome or gene mapping, in the production of
 CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
 CC therapy. Polypeptides of the invention can be used to target drugs to a
 CC tumour, in assays to determine biological activity, to raise
 CC antibodies/elicite an immune response, to determine quantitative protein
 CC levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 CC diseases, nervous system disorders, and infection. The present sequence
 CC represents a protein of the invention

XX SQ Sequence 384 AA;

Query Match 95.0%; Score 530; DB 4; Length 384;
 Best Local Similarity 94.4%; Pred. No. 1.2e-32;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 DB 170 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 229
 QY 61 DRFGSGSGTDFLTISRLEPEDFVYVCOQYSSPCSFQGTKEIK 108
 DB 230 DRFGSGSGTDFLTISRLEPEDFVYVCOQYSSPTTFQGTKEIK 277

RESULT 6
 AAU14463
 ID AAU14463 standard; protein; 384 AA.
 AC AAU14463;
 XX 24-OCT-2001 (first entry)
 DE Human novel protein #334.
 XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 XX tissue regeneration; immune disorder.

OS Homo sapiens.
 XX WO200155437-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US002623.
 XX 25-JAN-2000; 2000US-00491404.
 XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;
 DR WPI; 2001-451939/48.
 XX N-PSDB; AAS22768.
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage.
 PS Example 4; Page 826-827; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or
 CC their active domains. The polypeptides, polynucleotides and antibodies
 CC raised against the polypeptides are used in a method of treatment of a
 CC mammal and prevention of disorders caused by the aberrant protein
 CC expression or activity. The polypeptides can be used as molecular weight
 CC markers, food supplements, and in antibody production. The polypeptides
 CC are used to identify compounds which bind to the polypeptides.
 CC Polynucleotides of the invention are used as probes and primers, for
 CC sequencing, for chromosome or gene mapping, in the production of
 CC recombinant proteins, and in generating anti-sense DNA or RNA and in gene
 CC therapy. Polypeptides of the invention can be used to target drugs to a
 CC tumour, in assays to determine biological activity, to raise
 CC antibodies/elicite an immune response, to determine quantitative protein
 CC levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 CC diseases, nervous system disorders, and infection. The present sequence
 CC represents a protein of the invention

XX SQ Sequence 384 AA;

Query Match 95.0%; Score 530; DB 4; Length 384;
 Best Local Similarity 94.4%; Pred. No. 1.2e-32;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 DB 170 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 229
 QY 61 DRFGSGSGTDFLTISRLEPEDFVYVCOQYSSPCSFQGTKEIK 108
 DB 230 DRFGSGSGTDFLTISRLEPEDFVYVCOQYSSPTTFQGTKEIK 277

RESULT 7
 AAU14461
 ID AAU14461 standard; protein; 384 AA.
 AC AAU14461;
 XX 24-OCT-2001 (first entry)
 DE Human novel protein #332.
 XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 XX tissue regeneration; immune disorder.

OS Homo sapiens.
 XX WO200155437-A2.

```

PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US002623.
XX
XX 25-JAN-2000; 2000US-00491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-451939/48.
XX
XX N-PSDB; AAS22765.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage.
XX
XX Example 4; Page 824-825; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human proteins or
XX their active domains. The polypeptides, polynucleotides and antibodies
XX raised against the polypeptides are used in a method of treatment of a
XX mammal and prevention of disorders caused by the aberrant protein
XX expression or activity. The polypeptides can be used as molecular weight
XX markers, food supplements, and in antibody production. The polypeptides
XX are used to identify compounds which bind to the polypeptides.
XX Polynucleotides of the invention are used as probes and primers, for
XX sequencing, for chromosome or gene mapping, in the production of
XX recombinant proteins, and in generating anti-sense DNA or RNA and in gene
XX therapy. Polypeptides of the invention can be used to target drugs to a
XX tumour, in assays to determine biological activity, to raise
XX antibodies/ elicit an immune response, to determine quantitative protein
XX levels, as tissue markers, and to isolate receptors or ligands
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
XX versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
XX diseases, nervous system disorders, and infection. The present sequence
XX represents a protein of the invention
XX
XX Sequence 384 AA;
XX
XX Query Match 95.0%; Score 530; DB 4; Length 384;
XX Best Local Similarity 94.4%; Pred. No. 1.2e-32;
XX Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
XX Db |||||
XX
XX QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQQYGGSSPCSGGQTKLEIK 108
XX Db |||||
XX
XX 230 DRFGSGSGTDFLTISRLEPEDFAVYCYQQYGGSSPTTFGGQTKVDIK 277
XX
XX
XX RESULT 8
XX AAU14464
XX ID AAU14464 standard; protein; 384 AA.
XX
XX AC AAU14464;
XX
XX XX
XX 24-OCT-2001 (first entry)
XX
XX DE Human novel protein #335.
XX
XX KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
XX immunomodulatory; cycostatic; neuroprotective; vulnerary; nootropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;

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thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
tissue regeneration; immune disorder.

Homo sapiens.

WO200155437-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US002623.

25-JAN-2000; 2000US-00491404.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-451939/48.

N-PSDB; AAS22765.

Isolated polypeptides useful for treating anti-inflammatory diseases,
nervous system disorders, and for regenerating bone and cartilage.

Example 4; Page 827; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or
their active domains. The polypeptides, polynucleotides and antibodies
raised against the polypeptides are used in a method of treatment of a
mammal and prevention of disorders caused by the aberrant protein
expression or activity. The polypeptides can be used as molecular weight
markers, food supplements, and in antibody production. The polypeptides
are used to identify compounds which bind to the polypeptides.

Polynucleotides of the invention are used as probes and primers, for
sequencing, for chromosome or gene mapping, in the production of
recombinant proteins, and in generating anti-sense DNA or RNA and in gene
therapy. Polypeptides of the invention can be used to target drugs to a
tumour, in assays to determine biological activity, to raise
antibodies/ elicit an immune response, to determine quantitative protein
levels, as tissue markers, and to isolate receptors or ligands.

Polypeptides of the invention may also be useful in treating platelet
disorders, stem cell disorders, regenerating bone, cartilage, tendon,
ligament and/or nerve tissue, wound healing, treating burns, promoting
the proliferation, differentiation and survival of stem cells, as a
contraceptive, treating osteoporosis and osteoarthritis, anaemia,
Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
diseases, nervous system disorders, and infection. The present sequence
represents a protein of the invention

Sequence 384 AA;

Query Match 95.0%; Score 530; DB 4; Length 384;
Best Local Similarity 94.4%; Pred. No. 1.2e-32;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
Db |||||

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQQYGGSSPCSGGQTKLEIK 108
Db |||||

RESULT 9
AAE38059
ID AAE38059 standard; protein; 108 AA.
XX
XX AC AAE38059;
XX

DT 06-NOV-2003 (first entry)
DE Human 17G1 CD30 antibody light chain variable domain (VL) protein.
XX Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; systemic sclerosis; Grave's disease; ALCL;
XX atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
XX acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
XX Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
XX adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;
XX Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
XX light chain variable domain; VL.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 24..35
XX /note= "Complementarity determining region (CDR) 1"
XX Region 51..57
XX /note= "Complementarity determining region (CDR) 2"
XX Region 90..98
XX /note= "Complementarity determining region (CDR) 3"
XX WO2003059282-A2.
XX 24-JUL-2003.
XX 07-JAN-2003; 2003WO-US000440.
XX 09-JAN-2002; 2002US-0347649P.
XX 19-AUG-2002; 2002US-0404427P.
XX 06-DEC-2002; 2002US-0431684P.
XX (MEDA-) MEDAREX INC.
XX Keller T, Graziano R, Tremi J;
XX WPI; 2003-598476/56.
XX N-PSDB; AAD57371.
XX New human monoclonal antibody that binds to human CD30, useful for
XX treating or preventing tumor or autoimmune disease, e.g., rheumatoid
XX arthritis.
XX Claim 18; Fig 8; 122pp; English.
XX The invention relates to human monoclonal antibody that binds to human
XX CD30. The antibody is useful for treating or preventing tumour or
XX autoimmune disease e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
XX Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,
XX chronic renal failure, acute infectious mononucleosis, herpes or HIV
XX (human immunodeficiency virus) virus-associated diseases. The antibody is
XX also useful for treating Hodgkin's disease, anaplastic large cell
XX lymphoma (ALCL), adult T cell lymphoma (ATL), angioimmunoblastic
XX lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity
XX based lymphomas, embryonal carcinomas, undifferentiated carcinomas of the
XX rhino-pharynx (e.g. Schmincke's tumour), Castleman's disease, Kaposi's
XX Sarcoma and other T-cell or B-cell lymphomas. The present sequence is
XX human CD30 antibody VL (light chain variable domain) protein
XX Sequence 108 AA;
XX Query Match 94.3%; Score 526; DB 6; Length 108;
XX Best Local Similarity 94.4%; Pred. No. 7,2e-33;
XX Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 1 EVLVTSQPTLSLSPGERATLSGCRASQSVSSSYLAWYQKPGQAPRLLIYATSRATGIP 60
DB 1 EVLVTSQPTLSLSPGERATLSGCRASQSVSSSYLAWYQKPGQAPRLLIYATSRATGIP 60
OY 61 DRFSGSGGTDFTLTISLLEPDAFYVYCCQYGGSSPWTFGQTKVEIK 108

DB 61 DRFSGSGGTDFTLTISLLEPDAFYVYCCQYGGSSPWTFGQTKVEIK 108
RESULT 10
ADA89268
ID ADA89268 standard; protein; 109 AA.
XX AC ADA89268;
XX DT 20-NOV-2003 (first entry)
XX DE Human antibody 3G3 light chain amino acid sequence SEQ ID NO:112.
XX immunoglobulin; Ig; heavy chain variable domain;
XX light chain variable domain; major histocompatibility complex; MHC;
XX gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
XX Cancer.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003070752-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005128.
XX 20-FEB-2002; 2002US-0358994P.
XX (DYAX-) DYAX CORP.
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX Hoogenboom HRJM, Reiter Y;
XX WPI; 2003-663847/62.
XX N-PSDB; ADA89267.
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain
XX and an immunoglobulin light chain variable (VL) domain, useful for
XX preparing a composition for treating or preventing a cancerous disorder.
XX Disclosure; Fig 27A; 224pp; English.
XX The present invention describes a protein comprising an immunoglobulin
XX (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
XX domain. The protein binds a complex comprising a major histocompatibility
XX complex (MHC) and a peptide, does not substantially bind the MHC in the
XX absence of the bound peptide, and does not substantially bind the peptide
XX in the absence of the MHC. The peptide is a peptide fragment of gp100,
XX MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
XX comprising the novel protein and a carrier; (2) a cytotoxic T cell
XX comprising one or more nucleic acids for expressing the Ig that binds a
XX complex having an MHC and a peptide, does not substantially bind the MHC
XX in the absence of the bound peptide, and does not substantially bind the
XX peptide in the absence of the MHC; (3) an isolated nucleic acid
XX comprising a first segment that encodes the Ig variable domain; (4) a
XX host cell comprising heterologous nucleic acid sequences that encodes the
XX novel protein; (5) a transgenic animal whose genome includes heterologous
XX nucleic acid sequences that encode the protein; (6) identifying the
XX protein that specifically binds the MHC-peptide complex; (7) expressing
XX an antigen-binding protein; (8) ablating or killing a target cell that
XX displays a peptide on a surface MHC molecule; (9) treating or preventing
XX a cancerous disorder in a subject; and (10) detecting an MHC-peptide
XX complex in a sample. A protein of the invention has cytostatic activity,
XX and can be used in gene therapy. The protein is useful for preparing a
XX composition for treating or preventing a cancerous disorder. The present
XX sequence represents the light chain of an antibody which binds to an MHC-
XX peptide complex where the peptide component in as peptide fragment of
XX hTERT.
XX SQ Sequence 109 AA;
XX Query Match 94.3%; Score 526; DB 6; Length 109;

Best Local Similarity 94.4%; Pred. No. 7.3e-33;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60
Db 1 ETTLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYQYSSPCSFQGTKEIK 108
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYQYSSPVTFGQGTKEIK 108

RESULT 11
ABP57366
XX ID ABP57366 standard; protein; 131 AA.
XX AC ABP57366;
XX DT 22-APR-2003 (first entry)
XX DE Anti-TRAIL-R antibody related clone H-48-2 protein SEQ ID NO:27.
XX KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
XX KW antibody therapy.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200294880-A1.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-JP004816.
XX PR 18-MAY-2001; 2001JP-00150213.
XX PR 09-AUG-2001; 2001JP-00243040.
XX PR 11-OCT-2001; 2001JP-00314489.
XX PA (KIRI) KIRIN BEER KK.
XX PI Mori E, Kataoka S;
XX WPI; 2003-120790/11.
XX DR N-PSDB; ABZ59697.
XX DR N-PSDB;
XX PS New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
XX PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
XX PT nor inducing injury to hepatocytes, for use in therapy of malignant
XX PT tumor.
XX PS Claim 54; Page 59; 92pp; Japanese.
XX CC The present invention describes antibodies or their functional fragments
XX CC that bind to TRAIL-R1 and/or TRAIL-R2, TRAIL-R1 and TRAIL-R2 antibodies
XX CC have cytostatic and apoptotic activities, and can be used in antibody
XX CC therapy. The antibodies can be applied as remedies and preventives of
XX CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
XX CC in the therapy of malignant tumours. Remedies produced with the
XX CC antibodies are highly safe, and avoid hepatotoxicity. The present
XX CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
XX CC present invention
XX SQ Sequence 131 AA;
Query Match 94.2%; Score 525.5; DB 6; Length 131;
Best Local Similarity 95.4%; Pred. No. 9.4e-33;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYQYSSPCSFQGTKEIK 108

Db 81 DRFSGSGGTDTLTISRLEPEDFAVYCCQYQYSSPVTFGQGTKEIK 129

RESULT 12
ABG32514
XX ID ABG32514 standard; protein; 109 AA.
XX AC ABG32514;
XX DT 15-NOV-2002 (first entry)
XX DE Human VK region of monoclonal antibody for CD89, CD89 8.2 VK.
XX KW Human; monoclonal antibody; antibody; CD89; IGA receptor; Fcalpha;
XX KW light chain variable region; cancer; bacterial infection;
XX KW viral infection; parasitic infection; autoimmune disease; diabetes;
XX KW arthritis; multiple sclerosis; psoriasis; Crohn's disease; asthma;
XX KW allergies; chronic hepatitis; Henoch-Schonlein purpura; Berger's disease;
XX KW IGA-glomerulonephritis; CD89 8.2.
XX OS Homo sapiens.
XX PN WO200264634-A2.
XX PD 22-AUG-2002.
XX PF 11-FEB-2002; 2002WO-US004024.
XX PR 12-FEB-2001; 2001US-0268075P.
XX PR 05-NOV-2001; 2001US-0338956P.
XX PA (MEDA-) MEDAREX INC.
XX PI Hudson D, Van De Winkel J, Van Dijk MA;
XX WPI; 2002-643459/69.
XX DR N-PSDB; ABG52473.
XX DR N-PSDB;
XX PT New isolated human monoclonal antibody that binds to human CD89, useful
XX PT for in the treatment of diseases related to CD89 expression such as
XX PT cancer, bacterial, viral and parasitic infections and autoimmune
XX PT diseases.
XX PS Claim 10; Fig 4; 82pp; English.
XX CC The invention relates to an isolated human monoclonal antibody which
XX CC binds to human CD89 (an IGA receptor also called Fcalpha), comprising at
XX CC least one characteristic selected from: (i) a binding equilibrium
XX CC association constant (K_a) to human CD89 of at least about 10⁷M⁻¹; or
XX CC (ii) a dissociation constant (K_d) from human CD89 of about 10⁻⁸S⁻¹ or
XX CC less; (iii) absence of in vivo complement activation upon binding to
XX CC human CD89; (iv) the antibody binds to an epitope on human CD89 which
XX CC does not inhibit human IGA binding to the receptor; and (v) the antibody
XX CC comprises heavy chain and light chain components and their encoding
XX CC nucleic acids appearing as AB52470-AB52473 and ABG32511-ABG32514. The
XX CC human antibodies of the present invention that modulates CD89 level,
XX CC blocks or inhibits IGA binding to CD89 are useful in the treatment of
XX CC diseases related to CD89 expression or by circulating IGA-containing
XX CC complexes such as cancer, bacterial, viral and parasitic infections,
XX CC autoimmune diseases (diabetes, arthritis, multiple sclerosis, psoriasis,
XX CC Crohn's disease, asthma, and allergies), chronic hepatitis, Henoch-
XX CC Schonlein purpura, Berger's disease or IGA-glomerulonephritis. The
XX CC present sequence represents the light chain variable region of the
XX CC monoclonal antibody CD89 8.2
XX SQ Sequence 109 AA;
Query Match 94.0%; Score 524.5; DB 5; Length 109;
Best Local Similarity 95.4%; Pred. No. 9.5e-33;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYCOQKPGQAPRLIYATSSRATGIP 60

CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 226 AA;

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 1.9e-32;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSS-PCSFQGGTKLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPPYTFGGTKLEIK 109

RESULT 15
AAB75007
ID AAB75007 standard; protein; 226 AA.
XX
XX AAB75007;
XX
XX 19-JUL-2001 (first entry)
XX
XX Anti-IL8 monoclonal antibody protein fragment M1_23L.
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal.
KW
XX Homo sapiens.
OS Synthetic.
OS
XX WO200125492-A1.
PN
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027237.
XX
XX 02-OCT-1999; 99US-0157415P.
PR
XX 01-DEC-1999; 99US-00453234.
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
XX Buechler J, Valkirs G, Gray J, Lonberg N;
PI
XX WPI; 2001-335567/35.
DR
XX

PT Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
XX Example 22; Page 98; 161pp; English.

XX The present invention describes a method (M1) for producing a human
XX antibody phage display library (I), comprising: (1) providing a nonhuman
XX transgenic animal (II) whose genome comprises human immunoglobulin genes;
XX (2) isolating nucleic acids encoding human antibody chains (III) from
XX lymphatic cells; and (3) forming a library of display packages whose
XX members comprise a nucleic acid encoding (III) which is displayed from
XX the package. The method is used for producing a human antibody display
XX library, e.g., a Fab phage display library. The display method may be
XX used to screen nucleic acids encoding antibody chains obtained from
XX immunised nonhuman transgenic animals, and from this a population of
XX antibodies may be prepared. Production of a human monoclonal antibodies
XX display library using this method means there is no need to immunise
XX humans with antigens and the difficulties faced with immortalising B
XX cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
XX represent sequences used in the exemplification of the present invention

XX
SQ Sequence 226 AA;

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 1.9e-32;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSS-PCSFQGGTKLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPPYTFGGTKLEIK 109

Search completed: April 21, 2004, 17:01:54
Job time : 49.279 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:03:52 ; Search time 35.691 Seconds
(without alignments)
836.607 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558
Sequence: 1 EIVLTQSPGTLSSPGERAT.....CQYGSFPCFGQGTGLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	100.0	108	US-10-041-860-49	Sequence 49, Appl
2	558	100.0	108	US-10-041-860-225	Sequence 225, App
3	558	100.0	108	US-10-041-860-259	Sequence 259, App
4	558	100.0	108	US-10-041-860-375	Sequence 375, App
5	533	95.5	108	US-10-309-762-156	Sequence 156, App
6	532	95.3	108	US-10-307-724-123	Sequence 123, App
7	532	95.3	215	US-10-307-724-122	Sequence 122, App
8	530	95.0	384	US-10-291-265-805	Sequence 804, App
9	530	95.0	384	US-10-231-265-805	Sequence 805, App
10	530	95.0	384	US-10-231-265-806	Sequence 806, App
11	530	95.0	384	US-10-231-265-807	Sequence 807, App
12	529	94.8	108	US-10-269-711-21	Sequence 21, Appl
13	528	94.6	108	US-09-948-939-9	Sequence 9, Appli
14	526	94.3	108	US-10-338-366-4	Sequence 4, Appli
15	526	94.3	109	US-10-371-942-112	Sequence 112, App

16	525	94.1	106	15	US-10-309-762-163	Sequence 163, App
17	525	94.1	108	14	US-10-127-890-150	Sequence 150, App
18	524.5	94.0	109	14	US-10-073-644C-8	Sequence 8, Appli
19	524.5	94.0	226	10	US-09-453-234-50	Sequence 50, Appl
20	524.5	94.0	226	10	US-09-453-234-86	Sequence 86, Appl
21	524	93.9	108	15	US-10-309-762-43	Sequence 43, Appl
22	523	93.7	108	12	US-10-292-088-113	Sequence 113, App
23	522.5	93.6	109	14	US-10-223-880-8	Sequence 8, Appli
24	522	93.5	108	12	US-09-948-939-7	Sequence 7, Appli
25	522	93.5	109	12	US-10-371-942-64	Sequence 64, Appl
26	521	93.4	235	14	US-10-153-382-7	Sequence 7, Appli
27	520.5	93.3	109	12	US-10-251-085B-135	Sequence 135, App
28	520	93.2	108	14	US-10-269-805-32	Sequence 32, Appl
29	520	93.2	108	14	US-10-269-805-36	Sequence 36, Appl
30	518.5	92.9	109	12	US-10-251-085B-133	Sequence 133, App
31	518.5	92.9	226	10	US-09-453-234-80	Sequence 80, Appl
32	518.5	92.9	236	9	US-09-859-053-34	Sequence 34, Appl
33	518	92.8	108	10	US-09-848-788-178	Sequence 178, App
34	516	92.5	109	14	US-10-067-800-70	Sequence 70, Appl
35	514	92.1	109	12	US-10-371-942-104	Sequence 104, App
36	513.5	92.0	236	9	US-09-859-053-38	Sequence 38, Appl
37	513	91.9	108	12	US-10-180-648-14	Sequence 14, Appl
38	513	91.9	235	12	US-10-180-648-4	Sequence 4, Appli
39	512.5	91.8	108	12	US-10-371-942-36	Sequence 36, Appl
40	512.5	91.8	226	10	US-09-453-234-74	Sequence 74, Appl
41	512	91.8	108	15	US-10-309-762-39	Sequence 39, Appl
42	511.5	91.7	226	10	US-09-453-234-42	Sequence 42, Appl
43	511	91.6	307	15	US-10-291-265-332	Sequence 332, App
44	511	91.6	312	15	US-10-291-265-334	Sequence 334, App
45	510	91.4	108	14	US-10-041-860-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-041-860-49
; Sequence 49, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyan
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EIVLTQSPGTLSSPGERATLSCRASQSVSSSYLAWYQKQCAPRLITYATSSRATGIP	60
Db	1	EIVLTQSPGTLSSPGERATLSCRASQSVSSSYLAWYQKQCAPRLITYATSSRATGIP	60
Qy	61	DRFSGSGSGTDFTLTISRLEPEDFAVYTCQQYGGSSPCFSGQGTGLEIK	108
Db	61	DRFSGSGSGTDFTLTISRLEPEDFAVYTCQQYGGSSPCFSGQGTGLEIK	108

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RESULT 2
US-10-041-860-225
; Sequence 225, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-225

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108
DB 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108

RESULT 3
US-10-041-860-259
; Sequence 259, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108
DB 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108

```

```

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108
DB 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108

RESULT 4
US-10-041-860-375
; Sequence 375, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

Query Match 100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60
DB 1 EVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108
DB 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPFCFGQGTKLEIK 108

RESULT 5
US-10-309-762-156
; Sequence 156, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT FILING DATE: 2002-12-02
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-156

Query Match 95.5%; Score 533; DB 15; Length 108;
Best Local Similarity 95.4%; Pred. No. 2.8e-41;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy	1	EIVLTOSPCTLSLSPGERATLSGRASQSVSSSYLAWYQKQPCQAPRLLIYATSSRATGIP	60
Db	1	EIVLTOSPCTLSLSPGERATLSGRASQSVSSSYLAWYQKQPCQAPRLLIYATSSRATGIP	60
Qy	61	DRFSGSGSGDFTLTISRLEPEFAVYVYQYQYSSPCSFQGTQLEIK	108
Db	61	DRFSGSGSGDFTLTISRLEPEFAVYVYQYQYSSPITFGQTRLEIK	108

RESULT 6

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US-10-307-724-123
; Sequence 123, Application US/10307724
; Publication No. US2003023972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain variable region
US-10-307-724-123

```

```

Query Match      95.3%; Score 532; DB 15; Length 108;
Best Local Similarity 95.4%; Pred.No. 3.5e-41;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVILTQSPGTLTSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYATTSRATGIP 60
Db 1 EVILTQSPGTLTSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYATTSRATGIP 60

QY 61 DRFGSGSGGTFTLTISRLEPEDPAVYYCOQYGSSSPCSFGQTGLEIK 108
Db 61 DRFGSGSGGTFTLTISRLEPEDPAVYYCOQYGSSSPWTFGQTKVEIK 108

```

RESIST. 7

US-10-307-724-122
; Sequence 122, Application US/10307724
; Publication No. US2003032972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 215
; TYPE: PR1
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain
US-10-307-724-122

```

```

Query Match      95.3%; Score 532; DB 15; Length 215;
Best Local Similarity 95.4%; Pred. No. 7.1e-4;
Matches 103; Conservative 2; Mismatches 3; Indels 0

Qy 1 EIVLTQSPGTSLSPGERATISCRASQSVSSSYLAWYQQKPGQAPRLIIVAT
Db 1 EIVLTQSPGTSLSPGERATISCRASQSVSSSYLAWYQQKPGQAPRLIIVAT
Qy 61 DRFGSGGGSDPTLLIISLRLEPEDFAVYVYQYQSGSPSCFGQTKLEIK 108
Db 61 DRFGSGGGSDPTLLIISLRLEPEDFAVYVYQYQSGSPMTFGQTKVEIK 108

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RESULTS

```

US-10-291-265-804
; Sequence 804, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291.265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 804
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-804

```

Query Match 95.0%; Score 530; DB.15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYVATSRATGIP 60
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYVATSRATGIP 229

Qy 61 DRFGSGSGTDFLTITSLRLEPEFAVYICQYQSGSSPCFQGGKLEIK 108
Db 230 DRFGSGSGTDFLTITSLRLEPEFAVYICQYQSGSTTFQGGKVDIK 277

RESIST. 9

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; RESULT 3
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25

```

```
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

Query Match          95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 229
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 230 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVDIK 277
   |||||

RESULT 10
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-806

Query Match          95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 229
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 230 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVDIK 277
   |||||

RESULT 11
US-10-291-265-807
; Sequence 807, Application US/10291265
; Publication No. US20030232054A1
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 807
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-807

Query Match          95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 170 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 229
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 230 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVDIK 277
   |||||

RESULT 12
US-10-269-711-21
; Sequence 21, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989, US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-21

Query Match          94.8%; Score 529; DB 12; Length 108;
Best Local Similarity 94.4%; Pred. No. 6.5e-41;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 60
   |||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAQYQKPGQAPRLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKLEIK 108
   |||||
Db 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPGCGTKVBEIK 108
   |||||
```

```
RESULT 13
US-09-948-939-9
; Sequence 9, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Kortman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lomborg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
; OTHER INFORMATION: 4B6 from V $\kappa$  A-27
US-09-948-939-9

Query Match          94.6%; Score 528; DB 12; Length 108;
Best Local Similarity 94.4%; Pred. No. 9e-41;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPCSFGQGTKLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGQGTKVEIK 108

RESULT 14
US-10-338-366-4
; Sequence 4, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Graziano, Robert
; APPLICANT: Trembl, John
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-4

Query Match          94.3%; Score 526; DB 15; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.2e-40;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPCSFGQGTKLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGQGTKVEIK 108

RESULT 15
US-10-371-942-112
; Sequence 112, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-112

Query Match          94.3%; Score 526; DB 12; Length 109;
Best Local Similarity 94.4%; Pred. No. 1.2e-40;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPCSFGQGTKLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGQGTKLEIK 108

Search completed: April 21, 2004, 17:13:23
Job time : 36.691 secs
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:00:06 ; Search time 15.2961 Seconds
(without alignments)
364.511 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLSPGERAT.....CQYGSFPCFGQTKLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	95.0	108	2	US-08-232-081B-42
2	529	94.8	109	4	US-09-025-769B-16
3	525	94.1	108	1	US-08-488-113B-150
4	525	94.1	108	1	US-08-477-484B-150
5	525	94.1	108	2	US-08-646-360-150
6	525	94.1	108	3	US-08-839-765-150
7	525	94.1	108	3	US-09-136-389-150
8	525	94.1	108	4	US-09-610-838-150
9	525	94.1	108	4	US-09-711-485-150
10	524.5	94.0	226	4	US-09-456-090A-50
11	524.5	94.0	226	4	US-09-456-090A-86
12	521	93.4	235	4	US-09-472-087-14
13	521	93.4	235	4	US-09-472-087-65
14	518.5	92.9	226	4	US-09-456-090A-80
15	518	92.8	108	3	US-09-240-274-178
16	512.5	91.8	226	4	US-09-456-090A-74
17	511.5	91.7	226	4	US-09-456-090A-42
18	511	91.6	129	2	US-08-480-774A-4
19	508	91.0	108	1	US-07-634-278-86
20	508	91.0	108	1	US-08-477-728-86
21	508	91.0	108	1	US-08-474-040-86
22	508	91.0	108	1	US-08-487-200-86
23	508	91.0	108	3	US-08-484-537-86
24	506.5	90.8	226	4	US-09-456-090A-72
25	506	90.7	107	4	US-08-635-109-7
26	505	90.5	150	3	US-08-862-124-5
27	505	90.5	287	3	US-08-862-124-17

28	505	90.5	304	3	US-08-862-124-14	Sequence 14, Appl
29	504.5	90.4	107	1	US-08-107-669D-14	Sequence 14, Appl
30	504.5	90.4	107	1	US-08-472-789A-14	Sequence 14, Appl
31	504.5	90.4	107	2	US-08-477-531B-14	Sequence 14, Appl
32	504.5	90.4	107	2	US-08-082-842A-14	Sequence 14, Appl
33	504.5	90.4	226	4	US-09-456-090A-38	Sequence 38, Appl
34	500.5	89.7	224	4	US-09-456-090A-52	Sequence 52, Appl
35	499	89.4	141	4	US-09-472-087-88	Sequence 88, Appl
36	497	89.1	108	1	US-08-276-852-99	Sequence 99, Appl
37	497	89.1	108	1	US-08-899-575-99	Sequence 99, Appl
38	497	89.1	108	1	US-08-899-575-99	Sequence 99, Appl
39	497	89.1	108	5	PCT-US95-08743-99	Sequence 99, Appl
40	495.5	88.8	234	4	US-09-472-087-17	Sequence 17, Appl
41	495.5	88.8	234	4	US-09-472-087-69	Sequence 69, Appl
42	495	88.7	108	1	US-08-276-852-86	Sequence 86, Appl
43	495	88.7	108	1	US-08-899-575-86	Sequence 86, Appl
44	495	88.7	108	1	US-08-899-575-86	Sequence 86, Appl
45	495	88.7	108	5	PCT-US95-08743-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-08-232-081B-42
; Sequence 42, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-232-081B-42

Query Match 95.0%; Score 530; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 1,1e-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Cq 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60

QY 61 DRFGSGSGTDTLTISRLPEDFAVYCCQVSSPCSFQGTGKLEIK 108
 |||||
 Db 61 DRFGSGSGTDTLTISRLPEDFAVYCCQVSSPLTFGGQTKVEIK 108
 |||||

RESULT 2

US-09-025-769B-16
 ; Sequence 16, Application US/09025769B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 109 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-025-769B-16

Query Match 94.8%; Score 529; DB 4; Length 109;
 Best Local Similarity 94.4%; Pred. No. 1.4e-42;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPQLLIYATSSRATGIP 60
 |||||
 Db 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPQLLIYATSSRATGIP 60
 |||||
 QY 61 DRFGSGSGTDTLTISRLPEDFAVYCCQVSSPCSFQGTGKLEIK 108
 |||||
 Db 61 DRFGSGSGTDTLTISRLPEDFAVYCCQVSSPLTFGGQTKVEIK 108
 |||||

RESULT 3

US-08-488-113B-150
 ; Sequence 150, Application US/08488113B
 ; Patent No. 5744580
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; Proteins
 ; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,113B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-488-113B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
 Best Local Similarity 94.4%; Pred. No. 3.3e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPQLLIYATSSRATGIP 60
 |||||
 Db 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPQLLIYATSSRATGIP 60
 |||||
 QY 61 DRFGSGSGTDTLTISRLPEDFAVYCCQVSSPCSFQGTGKLEIK 108
 |||||
 Db 61 DRFGSGSGTDTLTISRLPEDFAVYCCQVSSPLTFGGQTKVEIK 108
 |||||
 RESULT 4
 US-08-477-484B-150
 ; Sequence 150, Application US/08477484B
 ; Patent No. 5756599
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-477-484B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGDTFTLTISRLEPDPFAVYCCQYGGSPCSFGQGTKEIK 108
Db 61 DRFSGSGGDTFTLTISRLEPDPFAVYCCQYGGSPXTFGQGTKEIK 108

RESULT 5
US-08-646-360-150
; Sequence 150, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-646-360-150

Query Match 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGDTFTLTISRLEPDPFAVYCCQYGGSPCSFGQGTKEIK 108
Db 61 DRFSGSGGDTFTLTISRLEPDPFAVYCCQYGGSPXTFGQGTKEIK 108

RESULT 6
US-08-839-765-150
; Sequence 150, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/839,765
 ; FILING DATE: 15-APR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-839-765-150

Query Match 94.1%; Score 525; DB 3; Length 108;
 Best Local Similarity 94.4%; Pred. No. 3.3e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
 Db 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
 QY 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYGSFQGTQKLEIK 108
 Db 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYGSFQGTQKLEIK 108

RESULT 7
 US-09-136-389-150
 ; Sequence 150, Application US/09136389
 ; Patent No. 6146850
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnicka, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/136,389
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/646,360
 ; FILING DATE: 13-MAY-1996
 ; APPLICATION NUMBER: PCT/US94/05348
 ; FILING DATE: 12-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 200-70.P4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-136-389-150

Query Match 94.1%; Score 525; DB 3; Length 108;
 Best Local Similarity 94.4%; Pred. No. 3.3e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
 Db 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
 QY 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYGSFQGTQKLEIK 108
 Db 61 DRFGSGSGTDFLTISRLEPGDFAVYVYCOQYGSFQGTQKLEIK 108

RESULT 8
 US-09-610-838-150
 ; Sequence 150, Application US/09610838
 ; Patent No. 6376217
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnicka, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173

; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-150

Query Match 94.1%; Score 525; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPDPFVYVYCOQYGGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPDPFVYVYCOQYGGSPXTFGQGTKEIK 108

RESULT 9
US-09-711-485-150
; Sequence 150, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-150

Query Match 94.1%; Score 525; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPDPFVYVYCOQYGGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPDPFVYVYCOQYGGSPXTFGQGTKEIK 108

RESULT 10
US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff

APPLICANT: Lomberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 50
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 8.3e-42;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSS-PCSFQGGTKLEIK 108
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSSPPYTFGGTKLEIK 109

RESULT 11
US-09-456-090A-86
Sequence 86, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lomberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 86
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match 94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 8.3e-42;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSS-PCSFQGGTKLEIK 108
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSSPPYTFGGTKLEIK 109

RESULT 12
US-09-472-087-14
Sequence 14, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-14

Query Match 93.4%; Score 521; DB 4; Length 235;
Best Local Similarity 91.7%; Pred. No. 1.8e-41;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSSPCSFQGGTKLEIK 108
Db 81 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSGTSPWTFGGTKVEIK 128

RESULT 13
US-09-472-087-65
Sequence 65, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 65
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-65

Query Match 93.4%; Score 521; DB 4; Length 235;
Best Local Similarity 91.7%; Pred. No. 1.8e-41;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSSPCSFQGGTKLEIK 108
Db 81 DRFSGSGGTDTLTISRLEPEDFAVYYCQQYSGTSPWTFGGTKVEIK 128

RESULT 14
US-09-456-090A-80
Sequence 80, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe

; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lombers, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-20L
US-09-456-090A-80

Query Match 92.9%; Score 518.5; DB 4; Length 226;
Best Local Similarity 93.6%; Pred. No. 3e-41;
Matches 102; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVMTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASRRATGIP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYYCQYQSGSPC-SFGQGTKLEIK 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYYCQYQSGSPMYTFGQGTKLEIK 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-09-240-274-178
; Sequence 178, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09S96-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-178

Query Match 92.8%; Score 518; DB 3; Length 108;
Best Local Similarity 94.3%; Pred. No. 1.5e-41;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIPDRF 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 LTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASRRATGIPDRF 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 64 SGSGSGTDFTLTISRLEPEDFAVYYCQYQSGSPCSPFGQGTKLEIK 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFTLTISRLEPEDFAVYYCQYQSGSPFTFGQGTKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: April 21, 2004, 17:05:19
Job time : 16.2961 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:58:51 ; Search time 9.73391 Seconds
(without alignments)
577.731 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLISLSPGERAT.....CQYGSPPCSFGQGTKLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528	94.6	129	1 KV3L HUMAN	P18135 homo sapien
2	526	94.3	129	1 KV3M HUMAN	P18136 homo sapien
3	524	93.9	109	1 KV3D HUMAN	P01622 homo sapien
4	521	93.4	109	1 KV3B HUMAN	P01620 homo sapien
5	508	91.0	109	1 KV3E HUMAN	P01623 homo sapien
6	503	90.1	108	1 KV3A HUMAN	P01619 homo sapien
7	500	89.6	109	1 KV3G HUMAN	P04206 homo sapien
8	466	83.5	100	1 KV3C HUMAN	P01621 homo sapien
9	465.5	83.4	128	1 KV3K HUMAN	P06311 homo sapien
10	446	79.9	109	1 KV3F HUMAN	P01624 homo sapien
11	439	78.7	129	1 KV3H HUMAN	P04207 homo sapien
12	420.5	75.4	115	1 KV3I HUMAN	P04433 homo sapien
13	415.5	74.5	114	1 KV4A HUMAN	P01625 homo sapien
14	414	74.2	116	1 KV3J HUMAN	P04434 homo sapien
15	399.5	71.6	134	1 KV4C HUMAN	P06314 homo sapien
16	397.5	71.2	108	1 KV1H HUMAN	P01600 homo sapien
17	387	69.4	133	1 KV4B HUMAN	P06313 homo sapien
18	382.5	68.5	108	1 KV1M HUMAN	P01605 homo sapien
19	380.5	68.2	108	1 KV1F HUMAN	P01598 homo sapien
20	379.5	68.0	108	1 KV1G HUMAN	P01603 homo sapien
21	375.5	67.3	129	1 KV1W HUMAN	P04431 homo sapien
22	374	67.0	113	1 KV2D HUMAN	P01617 homo sapien
23	373.5	66.9	108	1 KV1N HUMAN	P01606 homo sapien
24	373.5	66.9	108	1 KV1V HUMAN	P04430 homo sapien
25	371.5	66.6	111	1 KV3M MOUSE	P01665 mus musculus
26	370.5	66.4	108	1 KV1L HUMAN	P01604 homo sapien
27	369.5	66.2	111	1 KV3N MOUSE	P01666 mus musculus
28	369	66.1	107	1 KV1D HUMAN	P01596 homo sapien
29	367.5	65.9	111	1 KV3O MOUSE	P01667 mus musculus
30	366.5	65.7	111	1 KV3L MOUSE	P01664 mus musculus
31	365.5	65.5	108	1 KV1R HUMAN	P01610 homo sapien
32	365.5	65.5	111	1 KV3U MOUSE	P01673 mus musculus
33	364.5	65.3	108	1 KV1Y HUMAN	P00362 homo sapien

ALIGNMENTS

RESULT 1

KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.

AC P18135; 109 1 KV4D HUMAN

DT 01-NOV-1990 (Rel. 16, Created) 111 1 KV3Q_MOUSE

DT 01-NOV-1990 (Rel. 16, Last sequence update) 149 1 KV5A_MOUSE

DT 15-JUL-1999 (Rel. 38, Last annotation update) 108 1 KV1E_HUMAN

DB Ig kappa chain V-III region HAH precursor. 108 1 KV1G_HUMAN

OS Homo sapiens (Human). 111 1 KV3H_MOUSE

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; 117 1 KV2E_HUMAN

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 108 1 KV1O_HUMAN

OX NCBI_TaxID=9606; 108 1 KV1Q_HUMAN

RN [1] 129 1 KV4O_HUMAN

RP MEDLINE=88171307; PubMed=3127527; 108 1 KV1Q_MOUSE

RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.; 121 1 KV40_HUMAN

RT "Antibody-associated kappa light chain variable region gene 108 1 KV1B_HUMAN

RT expressed in chronic lymphocytic leukemia with little or no somatic 111 1 KV3S_MOUSE

RT mutation. Implications for etiology and immunotherapy."; 111 1 KV3S_MOUSE

RL J. Exp. Med. 167:840-852(1988). 111 1 KV3S_MOUSE

CC -I- DISEAS: the protein is one of the surface immunoglobulin M 111 1 KV3S_MOUSE

CC autoantibodies expressed in patients with chronic lymphocytic 111 1 KV3S_MOUSE

CC leukemia. 111 1 KV3S_MOUSE

CC PIR; P00022; K3HUHA. 111 1 KV3S_MOUSE

DR HSSP; P80362; 1WTL. 111 1 KV3S_MOUSE

DR GO: GO:0005576; C:extracellular; NAS. 111 1 KV3S_MOUSE

DR GO: GO:0003823; F:antigen binding; NAS. 111 1 KV3S_MOUSE

DR GO: GO:0008955; P:immune response; NAS. 111 1 KV3S_MOUSE

DR InterPro; IPR007110; IG-like. 111 1 KV3S_MOUSE

DR Pfam; PF00047; ig; 1. 111 1 KV3S_MOUSE

DR SMART; SM00406; IG; 1. 111 1 KV3S_MOUSE

DR PROSITE; PS50835; IG LIKE; 1. 111 1 KV3S_MOUSE

KW Immunoglobulin V region; Signal. 111 1 KV3S_MOUSE

FT SIGNAL 1 20 111 1 KV3S_MOUSE

FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH. 111 1 KV3S_MOUSE

FT DOMAIN 21 43 FRAMEWORK-1. 111 1 KV3S_MOUSE

FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1. 111 1 KV3S_MOUSE

FT DOMAIN 44 55 FRAMEWORK-2. 111 1 KV3S_MOUSE

FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING-2. 111 1 KV3S_MOUSE

FT DOMAIN 71 77 FRAMEWORK-3. 111 1 KV3S_MOUSE

FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-3. 111 1 KV3S_MOUSE

FT DOMAIN 110 118 JY1 SEGMENT. 111 1 KV3S_MOUSE

FT DOMAIN 119 139 BY SIMILARITY. 111 1 KV3S_MOUSE

FT DISULFID 43 109 111 1 KV3S_MOUSE

FT NON_TER 129 129 111 1 KV3S_MOUSE

SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64; 111 1 KV3S_MOUSE

Query Match 94.6%; Score 528; DB 1; Length 129;

Best Local Similarity 94.4%; Pred. No. 3.3e-48;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60

||||| 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 80

||||| 61 DRFGSGSGGTDFTLTITSLRLEPEDFAVYCYCQYGSPPCSFGQGTKLEIK 108

DB 81 DRFGSGSGTDFTLTISRLEPEDFAVYQQYGTSPRTFGQGTKEIK 128
|||||

RESULT 2

KV3D HUMAN
ID KV3D HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISAP: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.
CC PIR; PLOC021; K3HUHI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 94.3%; Score 526; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 5.3e-48;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAHYQQKPGAPRLIYATSSRATGIP 60
|||||
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAHYQQKPGAPRLIYATSSRATGIP 80
|||||
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQQYGTSPRTFGQGTKEIK 108
|||||
DB 81 DRFGSGSGTDFTLTISRLEPEDFAVYQQYGTSPRTFGQGTKEIK 128
|||||

RESULT 3

KV3D HUMAN
ID KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region Ti.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUHI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 7.1e-48;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAHYQQKPGAPRLIYATSSRATGIP 60
|||||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAHYQQKPGAPRLIYATSSRATGIP 60
|||||
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQQYGTSPRTFGQGTKEIK 108
|||||
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYQQYGTSPRTFGQGTKEIK 108
|||||

RESULT 4

KV3B HUMAN
ID KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUHI.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.

```
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 768993EBCD645FFB4 CRC64;

Query Match 93.4%; Score 521; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 1.5e-47;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQYSGSPQTFGQSKVEIK 108

RESULT 5
KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IGM anti-gamma-globulins of the wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HUWL.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0004955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E69CBEE CRC64;

Query Match 91.0%; Score 508; DB 1; Length 109;
Best Local Similarity 91.7%; Pred. No. 3.3e-46;
Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQYSGSLRGTFTGQTKVEIK 108

RESULT 6
KV3A HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR; A01893; K3HUGO.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0004955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 90.1%; Score 503; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.1e-45;
Matches 93; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 ZIVLTZSPGTLSPGZRAALSCASQSLSGYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGADFTLTISRLEZPEDFAVYCYQYSGSPFTFGQSKLEIK 108

RESULT 7
KV3G HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR; A01893; K3HUGO.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0004955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 90.1%; Score 503; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 1.1e-45;
Matches 93; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 ZIVLTZSPGTLSPGZRAALSCASQSLSGYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTKEIK 108
DB 61 DRFGSGSGADFTLTISRLEZPEDFAVYCYQYSGSPFTFGQSKLEIK 108
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SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;
Query Match 89.6%; Score 500; DB 1; Length 109;
Best Local Similarity 89.8%; Pred. No. 2.3e-45;
Matches 97; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
D 1 EIVLTQSPGTLSPGERATLSCRAALLSRGLAYWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYSSPSCFGQGTKEIK 108
D 61 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYSSPSCFGQGTKEIK 108

RESULT 8
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS; THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUN9.
DR HSP; P80362; 1WTI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0008955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Hybridoma.
FT SIGNAL 1
FT CHAIN <1 4
FT DOMAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 83.5%; Score 466; DB 1; Length 100;
Best Local Similarity 94.7%; Pred. No. 7.1e-42;
Matches 90; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
D 5 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 64
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYSS 95
D 65 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYSS 99

RESULT 9
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G.; Meindl A.; Combratio G.; Solomon A.; Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR HSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0008955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 83.4%; Score 465.5; DB 1; Length 128;
Best Local Similarity 87.0%; Pred. No. 1.1e-41;
Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
D 21 EIVLTQSPGTLSPGESATLSCRASQSVSSN-LAWYQKRGQSPRLIIIRDASSRANGIP 79
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYSSPSCFGQGTKEIK 108
D 80 DRFGSGSGTDFTLTISRLEPEDFAVYCYQYSSPSCFGQGTKEIK 127

RESULT 10
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -1- IMMUNELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR; A01897; KGHUPM.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW FT CHAIN 1 20
FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 79.9%; Score 446; DB 1; Length 109;
Best Local Similarity 78.7%; Pred. No. 9.6e-40;
Matches 85; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCASQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
DB 1 EIVTQSPVTLVSFGERATLSCASQSVSSSYLAWYQQKPGSGFRLLIYGASTRATGIP 60
QY 61 DRFGSGSGTDFTLTISLSEPEDFAVYCCQYGS-SPCSFGQTKLEIK 108
DB 61 ARFSGSGSGTFTLTISLSQSEDFAVYCCQYNNWPFVFGQTRVEIK 108

RESULT 11
KV3H_HUMAN STANDARD; PRT; 129 AA.
ID KV3H_HUMAN
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC
CC EMBL; M12740; AAA58992.1; -
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW FT CHAIN 1 20
FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION Vg.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 79.7%; Score 439; DB 1; Length 129;
Best Local Similarity 79.8%; Pred. No. 6.3e-39;
Matches 87; Conservative 11; Mismatches 9; Indels 2; Gaps 2;

QY 1 EIVLTQSPGTLISLSPGERATLSCASQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
DB 21 EIVTQSPATLVSFGERATLSCASQSVNN-LAWYQQKPGQAPRLIYGASTRATGIP 79
QY 61 DRFGSGSGTDFTLTISLSEPEDFAVYCCQYGS-SPCSFGQTKLEIK 108
DB 80 ARFSGSGSGTFTLTISLSQSEDFAVYCCQYNNWPFVFGQTRVEIK 128

RESULT 12
KV3I_HUMAN STANDARD; PRT; 115 AA.
ID KV3I_HUMAN
AC P0433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pach M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC
CC EMBL; X01668; -; NOT_ANNOTATED_CDS.
CC PIR; A01900; K3HUVG.
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT DOMAIN 21 >115 IG KAPPA CHAIN V-III REGION Vg.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
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FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DB47CDA3A17D555 CRC64;

Query Match 75.4%; Score 420.5; DB 1; Length 115;
Best Local Similarity 88.5%; Pred. No. 4.7e-37;
Matches 85; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSRATGIP 60
DB 21 EIVLTQSPATLSLSPGERATLSCRAQSV-SSYLAWYQKPGQAPRLIIYATSRATGIP 79
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSP 96
DB 80 ARFGSGSGTDFLTISRLEPEDFAVYCCQYGGSP 115

RESULT 13
KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1995 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seivler's Z. Physiol. Chem. 356:507-557 (1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1986) to Swiss-Prot.
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1EEQ; 01-FEB-01.
DR PDB; 1ESU; 03-FEB-01.
DR PDB; 1ERQ; 09-FEB-01.
DR PDB; 1EX3; 06-MAR-01.
DR PDB; 1LVE; 21-JAN-98.
DR PDB; 3LVE; 18-MAY-99.
DR PDB; 5LVE; 28-MAR-01.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 74.5%; Score 415.5; DB 1; Length 114;
Best Local Similarity 84.4%; Pred. No. 2.2e-36;
Matches 81; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRAQSVSSSYLAWYQKPGQAPRLIIYATSRATGIP 60
DB 21 EIVLTQSPPTLSLSPGERVTLSCRAQSVSSSYLTWYQKPGQAPRLIIYATSRATGIP 80
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSP 96

Best Local Similarity 70.8%; Pred. No. 1.5e-36;
Matches 80; Conservative 16; Mismatches 12; Indels 5; Gaps 1;

QY 1 EIVLTQSPGTLISLSPGERATLSCRAQSV-----SSSYLAWYQKPGQAPRLIIYATSSR 55
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAQYQKPGQPPKLLIWTASTR 60
QY 56 ATGIDPRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPSCPSFGQGTLEIK 108
DB 61 ESGVPRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSTPYSPFGQGTLEIK 113

RESULT 14
KV30_HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236 (1984).
CC -----
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CC -----
CC EMBL; X02725; -; NOT ANNOTATED_CDS.
CC PIR; A01901; K3HUVH.
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 74.2%; Score 414; DB 1; Length 116;
Best Local Similarity 84.4%; Pred. No. 2.2e-36;
Matches 81; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 12.515 Seconds
(without alignments)
830.097 Million cell updates/sec

Title: US-10-041-860-49
Perfect score: 558
Sequence: 1 EIVLTQSPGTLSPGERAT.....CQQYGSFCSFGQGTKLEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191536 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	95.9	108	2	H30608
2	535	95.9	108	2	H30601
3	534	95.7	109	2	H30601
4	533	95.5	109	2	H30601
5	531	95.2	109	2	H30601
6	531	95.2	109	2	H30601
7	530	95.0	109	2	H30601
8	530	95.0	129	2	S46369
9	530	95.0	134	2	S38643
10	529	94.8	109	2	H30601
11	529	94.8	129	2	S49532
12	528	94.6	129	1	K3HUBA
13	527	94.4	128	2	S20636
14	526	94.3	129	1	K3HUBI
15	524	93.9	109	1	K3HUTI
16	524	93.9	109	2	H30601
17	523.5	93.8	114	2	S46375
18	521	93.4	109	1	K3HUSI
19	520	93.2	109	2	H30608
20	515	92.3	109	2	H30607
21	514	92.1	107	2	H30965
22	514	92.1	108	2	H30608
23	513	91.9	124	2	S20638
24	511	91.6	121	1	S40327
25	508	91.0	109	1	K3HURL
26	507	90.9	110	2	S20635
27	504.5	90.4	108	2	E30609
28	503.5	90.2	110	2	E30607
29	503	90.1	108	1	K3HUB6

RESULT 1
C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: C30608
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoant
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: C30608
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-108 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

ALIGNMENTS

RESULT 1

Query Match 95.9%; Score 535; DB 2; Length 108;
Best Local Similarity 96.3%; Pred. No. 5.3e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFCSFGQGTKLEIK 108
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSFCSFGQGTKLEIK 108

RESULT 2

H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: H30601; E30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotypic characterization of the L chains of human IgM autoant
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: H30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON1>
A/Accession: E30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON2>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 109;
 Best Local Similarity 96.3%; Pred. No. 5.3e-38;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCFGQGTKEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFYFGQGTKEIK 108

RESULT 3
 F30601
 Ig kappa chain V-III region (New) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C/Accession: F30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A/Reference number: A30601; MUID:89215279; PMID:2496160
 A/Accession: F30601
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMV>

Query Match 95.7%; Score 534; DB 2; Length 109;
 Best Local Similarity 93.5%; Pred. No. 6.5e-38;
 Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCFGQGTKEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPCTFGQGTKEIK 108

RESULT 4
 B30601
 Ig kappa chain V-III region (Glo) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C/Accession: B30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A/Reference number: A30601; MUID:89215279; PMID:2496160
 A/Accession: B30601
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMV>

Query Match 95.5%; Score 533; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 7.8e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCFGQGTKEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFYFGQGTKEIK 108

Db 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFTFGQGTKEIK 108

RESULT 5
 F0963
 Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
 C/Accession: F0963
 R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: F0952; MUID:92202880; PMID:1552291
 A/Accession: F0963
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-109 <VAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;1-23/Region: framework 1
 F;16-91/Domain: immunoglobulin homology <IMV>
 F;24-34/Region: complementarity-determining 1
 F;35-50/Region: framework 2
 F;51-56/Region: complementarity-determining 2
 F;57-89/Region: framework 3
 F;90-97/Region: complementarity-determining 3

Query Match 95.2%; Score 531; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 1.1e-37;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCFGQGTKEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPAFGQGTKEIK 108

RESULT 6
 D30601
 Ig kappa chain V-III region (Cur) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C/Accession: D30601
 R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
 J. Immunol. 142, 3158-3163, 1989
 A/Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A/Reference number: A30601; MUID:89215279; PMID:2496160
 A/Accession: D30601
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-109 <GON>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMV>

Query Match 95.2%; Score 531; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 1.1e-37;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFCFGQGTKEIK 108
 DB 61 DRFGSGSGTDFLTISRLEPEDFAVYCCQYGGSPFTFGQGTKEIK 108

RESULT 7
 C30601

IG kappa chain V-III region (Pay) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: C30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotype characterization of the L chains of human IgM autoantibodies.
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: C30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.4e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPCSFQGGTKLEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPLTFQGGTKVEIK 108

RESULT 8
S46369
IG light chain variable region (VJ) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46369
R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement.
A/Reference number: S46369; MUID:94313975; PMID:8039491
A/Accession: S46369
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <BEN>
A/Cross-references: EMBL:Z27170
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:136-111/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 129;
Best Local Similarity 95.4%; Pred. No. 1.6e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 80

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPCSFQGGTKLEIK 108
DB 81 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPFPFGGQTKLEIK 128

RESULT 9
S38643
IG kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38643
R/Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A/Reference number: S38643
A/Accession: S38643
A/Status: preliminary

A/Molecule type: mRNA
A/Residues: 1-134 <BEN>
A/Cross-references: EMBL:Z27170; NID:9415955; PIDN:CAA81694.1; PID:9415956
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:41-116/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 134;
Best Local Similarity 95.4%; Pred. No. 1.7e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 60
DB 26 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 85

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPCSFQGGTKLEIK 108
DB 86 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPFPFGGQTKLEIK 133

RESULT 10
G30601
IG kappa chain V-III region (Got) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C/Accession: G30601
R/Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A/Title: Structural and idiotype characterization of the L chains of human IgM autoantibodies.
A/Reference number: A30601; MUID:89215279; PMID:2496160
A/Accession: G30601
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <GON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.7e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKQPGQAPRLIIYATSSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPCSFQGGTKLEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCQYGGSSPFPFGGQTKLEIK 108

RESULT 11
S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C/Accession: S49532
R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S49532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <MAH>
A/Cross-references: EMBL:Z46345; NID:9560843; PIDN:CAA8464.1; PID:9560844
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 129;
Best Local Similarity 95.4%; Pred. No. 2e-37;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 EIVLTQSPGTLSPGGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 80
Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSSPCSFGQGTKEIK 108
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSSPQTFGQGTKEIK 128

RESULT 12
K3HUHA
Ig kappa chain precursor V-III region (Hah) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C:Accession: PLO022
R:Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A:Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A:Reference number: FLO021; MUID:8811307; PMID:3127527
A:Accession: PLO022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
C:Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAP>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted

Query Match 94.4%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.4e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 80
Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSSPCSFGQGTKEIK 108
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGSPRFTGQGTKEIK 128

RESULT 13
K3HUHA
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20636
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Reference number: S20631
A:Accession: S20636
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <LEE>
A:Cross-references: ENBL:Z11894; NUD:g33200; PIDN:CAA77948.1; PID:g33201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 527; DB 2; Length 128;

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A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-91/Domain: immunoglobulin homology <IMM>
F:23-89/Disulfide Bonds: #status predicted

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 4.4e-37;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVNSFLAWYQOKPGQAPRLIIYVASSRATGIP 60

QY 61 DRFSGSGGTDFTLTIISRLPEDEFAVYICQYQYSSPSPSGFGQTKLEIK 108
Db 61 DRFSGSGGTDFTLTIISRLPEDEFAVYICQYQYSSPSPSGFGQTKVELK 108

Search completed: April 21, 2004, 17:04:25
Job time : 13.515 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:00:06 ; Search time 17.7039 Seconds
(without alignments)
364.511 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672
Sequence: 1 QVQLVQGAEVKPGASVKV.....YDIYGMVWVGQTTTVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 399414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 399414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541.5	80.6	120	4	US-09-025-769B-36
2	541.5	80.6	120	4	US-09-025-769B-59
3	528	78.6	117	4	US-09-025-769B-22
4	513	76.3	125	3	US-09-199-149-3
5	510.5	76.0	128	1	US-08-202-047-22
6	510.5	76.0	128	3	US-08-964-690-22
7	510.5	75.9	129	2	US-08-561-521-45
8	510	75.9	129	4	US-08-525-539A-77
9	510	75.9	129	5	PCT-US95-01219-45
10	502	74.7	123	1	US-08-477-877B-94
11	502	74.7	123	2	US-08-472-281A-94
12	502	74.7	123	2	US-08-477-989B-94
13	501	74.6	119	2	US-08-561-521-10
14	501	74.6	119	5	PCT-US95-01219-10
15	498	74.1	119	4	US-09-438-954-41
16	496	73.8	117	3	US-08-545-809A-96
17	493.5	73.4	139	1	US-08-253-877C-19
18	493.5	73.4	139	2	US-08-452-164A-19
19	493.5	73.4	139	3	US-08-603-024-18
20	493.5	73.4	139	4	US-08-450-809-14
21	487	72.5	121	1	US-08-202-047-23
22	487	72.5	121	3	US-08-964-690-23
23	482	71.7	119	2	US-08-561-521-12
24	482	71.7	119	5	PCT-US95-01219-12
25	481	71.6	123	1	US-08-482-882-86
26	481	71.6	123	2	US-08-483-389-86
27	481	71.6	123	2	US-08-487-113D-86

ALIGNMENTS

RESULT 1

US-09-025-769B-36

; Sequence 36, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 120 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-025-769B-36

Query Match 80.6%; Score 541.5; DB 4; Length 120;

Best Local Similarity 84.0%; Pred. No. 1.4e-44;

Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

Sequence 86, Appl

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
 Db 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 115
 QY 121 VTVSS 125
 Db 116 VTVSS 120

RESULT 2

US-09-025-769B-59
 ; Sequence 59, Application US/09025769B
 ; Patent No. 6300064

GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 59:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-025-769B-59

Query Match 80.6%; Score 541.5; DB 4; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.4e-44;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
 Db 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 115
 QY 121 VTVSS 125

Db 116 VTVSS 120

RESULT 3

US-09-025-769B-22
 ; Sequence 22, Application US/09025769B
 ; Patent No. 6300064

GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 117 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-025-769B-22

Query Match 78.6%; Score 528; DB 4; Length 117;
 Best Local Similarity 82.5%; Pred. No. 2.6e-43;
 Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
 Db 61 AQKFGQGRVTMTSDTSISTAYMELSLRSDDTAVYYCARDG-----GFDYWGQGT 111
 QY 120 TVTVSS 125
 Db 112 LVTVSS 117

RESULT 4

US-09-199-149-3
 ; Sequence 3, Application US/09199149
 ; Patent No. 6160099
 ; GENERAL INFORMATION:

```
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen O.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Kabat VH subgroup I
US-09-199-149-3

Query Match:          76.3%; Score 513; DB 3; Length 125;
Best Local Similarity 80.6%; Pred. No. 7.5e-42;
Matches 104; Conservative 8; Mismatches 9; Indels 8; Gaps 5;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISNVRQAPGQGLEWMGWINP- 59
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSDTAIYICVR-GFGYS---YNYDYIYGMVDV 116
DB 60 AQKFGQRTVITADTSTSTAYMELSLRSDTAIYICARPGYGGGCGY-WYWG--VMG 116
QY 117 QGTTVTVSS 125
DB 117 QGTLTVSS 125

RESULT 5
US-08-202-047-22
; Sequence 22, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22

Query Match:          76.0%; Score 510.5; DB 1; Length 128;
Best Local Similarity 77.9%; Pred. No. 1.3e-41;
Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATQGLEWMGWINP-NSGNTD 59
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISNVRQAPGQGLEWMGWINPVGNDTN 60
QY 60 YAKFGQRTVMTDTSISTAYMELSLRSDTAIYICVRGFGYS-----YNYDYIYGMVDV 114
DB 61 YAKFGQRTVITADTSTSTAYMELSLRSDTAIYICARPGYGGGCGYRGRDYF---DY 117
QY 115 WGQGTITVSS 125
DB 118 WGQGTITVSS 125

RESULT 6
US-08-964-690-22
; Sequence 22, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22

Query Match 76.0%; Score 510.5; DB 3; Length 128;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYNGD 60
QY 60 YAAKFGQGRVTMTSDTSISTAYMELSLRSEDATYYCVRGFGYS-----YNDYYGMDV 114
Db 61 YAAKFGQGRVTITADTSTAYMELSLRSEDATYYCARAPGYGGGCGYRGDYF--DY 118
QY 115 WGQGTITVTSS 125
Db 119 WGQGLTLVTSS 129

RESULT 7
US-08-561-521-45
; Sequence 45 Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Legier, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-45

Query Match 75.9%; Score 510; DB 2; Length 129;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 14; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYNGD 60
QY 60 YAAKFGQGRVTMTSDTSISTAYMELSLRSEDATYYCVRGFGYS-----YNDYYGMDV 114
Db 61 YAAKFGQGRVTITADTSTAYMELSLRSEDATYYCARAPGYGGGCGYRGDYF--DY 118
QY 115 WGQGTITVTSS 125
Db 119 WGQGLTLVTSS 129

RESULT 8
US-08-525-539A-77
; Sequence 77 Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELETYPE: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-77

Query Match 75.9%; Score 510; DB 4; Length 129;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 14; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYNGD 60
QY 60 YAAKFGQGRVTMTSDTSISTAYMELSLRSEDATYYCVRGFGYS-----YNDYYGMDV 114
Db 61 YAAKFGQGRVTITADTSTAYMELSLRSEDATYYCARAPGYGGGCGYRGDYF--DY 118
QY 115 WGQGTITVTSS 125
Db 119 WGQGLTLVTSS 129
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RESULT 9
PCT-US95-01219-45
; Sequence 45, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-45

Query Match 75.9%; Score 510; DB 5; Length 129;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
Matches 102; Conservative 7; Mismatches 14; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWINP-NSGNTD 59
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWINP-NSGNTD 60
QY 60 YAKFQGRVTMTDRTSISTAYMELSSLRSEDTAIYVCVRGFGYS-----YNDYYVYGMGV 114
Db 61 YAKFQGRVTITADTSTSTAYMELSSLRSEDTAVYICARPGYSGSGGCGYRGDYP--DY 118
QY 115 WQGGTIVTVSS 125
Db 119 WQGGTIVTVSS 129

RESULT 10
US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-477-877B-94

Query Match 74.7%; Score 502; DB 1; Length 123;
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels 8; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWINP-NSGNTD 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWINP-NSGNTD 60
QY 61 AQKFGQGRVTMTDRTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYY-----GMDVWQ 117
Db 61 AQKFGQGRVTMTDRTSISTAYMELSSLRSEDTAVYICARPGYSGSGGCGYRGDYP--DY 118
QY 118 GTTVTVSS 125
Db 116 GTTVTVSS 123

RESULT 11
US-08-472-281A-94
; Sequence 94, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
```

STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-472-281A-94

Query Match 74.7%; Score 502; DB 2; Length 123;
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels 8; Gaps 2;
QY 1 QVQLVSGAEVKPGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTDY 60
Db 1 QVQLVSGAEVKPGASVKVSKASGYTFTGYMHWVRQAPQGLEWMGRINPNSGGINY 60
QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCVRFSGYSYNDYY---GMDVWGQ 117
Db 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCARG-----RTEYIVVAEGFDYWGQ 115
QY 118 GTTVTVSS 125
Db 116 GTLVTVSS 123

RESULT 12
US-08-477-989B-94
Sequence 94, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Postema, Christina B.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable
US-08-477-989B-94

Query Match 74.7%; Score 502; DB 2; Length 123;
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels 8; Gaps 2;
QY 1 QVQLVSGAEVKPGASVKVSKASGYTFTSDINWVRQATGQGLEWMGWNPNSGNTDY 60
Db 1 QVQLVSGAEVKPGASVKVSKASGYTFTGYMHWVRQAPQGLEWMGRINPNSGGINY 60
QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCVRFSGYSYNDYY---GMDVWGQ 117
Db 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYVCARG-----RTEYIVVAEGFDYWGQ 115
QY 118 GTTVTVSS 125
Db 116 GTLVTVSS 123

RESULT 13
US-08-561-521-10
Sequence 10, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561.521
FILING DATE: 25-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-10

Query Match 74.6%; Score 501; DB 5; Length 119;
Best Local Similarity 79.2%; Pred. No. 9.9e-41;
Matches 99; Conservative 7; Mismatches 13; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLRWGWINAGNGNTKY 60
QY 61 AQKFGQVRVTMTSDTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGIT 120
DB 61 SQKFGQVRVTITRDTASTAYMELSSLRSEDTAVIYCARG-GY-----YSGSGSNYGQGITL 114
QY 121 VTSS 125
DB 115 VTSS 119

RESULT 15
US-09-438-954-41
Sequence 41, Application US/09438954
Patent No. 6458934
GENERAL INFORMATION:
APPLICANT: HONG, Hyo Jeong
APPLICANT: PARK, Sung Sup
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yuil
APPLICANT: YOON, Sung Kwan
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
FILE REFERENCE: 1303-124P
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Variable
OTHER INFORMATION: region of heavy chain of human antibody (M17750)
US-09-438-954-41

Query Match 74.1%; Score 498; DB 4; Length 119;
Best Local Similarity 78.4%; Pred. No. 1.9e-40;
Matches 98; Conservative 8; Mismatches 13; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLRWGWINAGNGNTKY 60
QY 61 AQKFGQVRVTMTSDTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGIT 120

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561.521
FILING DATE: 25-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-10

Query Match 74.6%; Score 501; DB 2; Length 119;
Best Local Similarity 79.2%; Pred. No. 9.9e-41;
Matches 99; Conservative 7; Mismatches 13; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLRWGWINAGNGNTKY 60
QY 61 AQKFGQVRVTMTSDTSISTAYMELSSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGIT 120
DB 61 SQKFGQVRVTITRDTASTAYMELSSLRSEDTAVIYCARG-GY-----YSGSGSNYGQGITL 114
QY 121 VTSS 125
DB 115 VTSS 119

RESULT 14
PCT-US95-01219-10
Sequence 10, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219

Thu Apr 22 06:00:01 2004

Db 61 SOKFOGRVTITRDTASASTAYNELSLRSEDTAVVYCARG-GY-----YGSOSNYWGEGL 114
Qy 121 VTVSS 125
Db 115 VTVSS 119

Search completed: April 21, 2004, 17:05:18
Job time : 26.7039 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 16:55:26 ; Search time 54.721 Seconds

(without alignments)
645.427 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYIYGVMDVWGQGTITVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	561.5	83.6	122	ABR55829	Heavy cha
2	558.5	83.1	145	ABP57367	Anti-TRAI
3	553.5	82.4	126	ADA89120	MS-Pro-26
4	551	82.0	127	ADA89122	MS-Pro-29
5	547.5	81.5	128	ADA89202	Human ant
6	544	81.0	476	AAW88464	Monoclonal
7	542.5	80.7	126	ADA89116	MS-Pro-11
8	541.5	80.6	120	AAW27551	Human Ab
9	541	80.5	146	AAW22841	Human ant
10	538	80.1	136	ADD28330	Human het
11	537	79.9	203	AAV34301	IgM antib
12	536.5	79.8	126	ADA89123	MS-Pro-54
13	536.5	79.8	247	ABP45718	Human Bly
14	536	79.8	125	ABP55813	Heavy cha
15	534.5	79.5	118	ADA89115	MS-Pro-2
16	534.5	79.5	249	ABP44908	Human Bly
17	533	79.3	245	AAAB67619	Human leu
18	532.5	79.2	230	ABR01514	Human ant
19	529.5	78.8	120	ABJ18719	Antibody
20	529.5	78.8	120	ABJ18673	Antibody
21	527.5	78.5	146	AAAB53510	Human col
22	526.5	78.3	228	ABR01526	Human ant
23	526	78.3	199	AAV34302	IgM antib
24	526	78.3	470	AAU74296	Anti-huma
25	524.5	78.1	245	ABP45885	Human Bly

26	524	78.0	255	5	ABP45396	Human Bly
27	523.5	77.9	247	5	ABP44916	Human Bly
28	523.5	77.9	247	5	ABP44937	Human Bly
29	521.5	77.6	126	6	ADA89124	MS-Pro-55
30	520	77.4	256	5	ABP45290	Human Bly
31	519.5	77.3	251	5	ABP45910	Human Bly
32	518.5	77.2	120	6	ABR55815	Heavy cha
33	518.5	77.2	238	5	ABP45896	Human Bly
34	518	77.1	120	4	AAAB62747	Human HIV
35	517.5	77.0	116	5	ABR57555	HLA-DR-5p
36	517.5	77.0	249	5	ABP45624	Human Bly
37	515.5	76.7	249	5	ABP45279	Human Bly
38	515.5	76.7	249	5	ABP45288	Human Bly
39	515.5	76.7	252	5	ABP45864	Human Bly
40	515	76.6	251	5	ABR45795	Human Bly
41	514	76.5	221	6	ABR01537	Human ant
42	513.5	76.4	241	5	ABP46020	Human Bly
43	513	76.3	125	3	AAV71447	Human hea
44	512	76.2	248	5	ABP45710	Human Bly
45	511.5	76.1	249	5	ABP44915	Human Bly

ALIGNMENTS

RESULT 1

ABR55829
ID: ABR55829 standard; protein; 122 AA.

AC ABR55829;

DT 02-SEP-2003 (first entry)

DE Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC.

KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antiprosoritic; cancer;
KW angiogenesis; antibody.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Region 26..36 /note= "complementarity determining region (CDR) 1"

FT Region 50..66 /note= "complementarity determining region (CDR) 2"

FT Region 96..112 /note= "complementarity determining region (CDR) 3"

XX WO2003030833-A2.

XX 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032613.

XX 11-OCT-2001; 2001US-0328604P.

XX 10-OCT-2002; 2002US-00269905.

XX (AMGE-) AMGEN INC.

XX Oliner JD;

XX WPI; 2003-504963/47.

XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

XX Claim 1; Page 93; 161pp; English.

XX The invention relates to a specific binding agent, which comprises at
XX least one peptide selected from any of 62 peptides (ABR55789-830) or its
XX fragment. The binding agents are antibodies that recognize and bind to

CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
 CC antibody, is useful for inhibiting undesired angiogenesis, treating
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
 CC 2 activity, modulating vascular permeability or plasma leakage, or
 CC treating a disease (e.g. ocular neovascular disease, obesity,
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
 CC disease, bone-related disease, or psoriasis) in a mammal. The present
 CC sequence represents a heavy chain variable region of an anti-Ang-2
 CC antibody
 XX
 SQ Sequence 122 AA;

Query Match 83.6%; Score 561.5; DB 6; Length 122;
 Best Local Similarity 86.4%; Pred. No. 3.2e-44;
 Matches 108; Conservative 5; Mismatches 9; Indels 3; Gaps 1;
 QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 DB 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
 QY 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGY-SYNDYYGMDVWGQGT 120
 DB 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCAKEIAVA---GTRYGMDVWGQGT 117
 QY 121 VTVSS 125
 DB 118 VTVSS 122

RESULT 2
 ABP57367
 ID ABP57367 standard; protein; 145 AA.
 XX AC ABP57367;
 XX DT 22-APR-2003 (first entry)
 XX DE Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.
 XX KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
 XX KW antibody therapy.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200294880-A1.
 XX PD 28-NOV-2002.
 XX PF 17-MAY-2002; 2002WO-JP004816.
 XX PR 18-MAY-2001; 2001JP-00150213.
 XX PR 09-AUG-2001; 2001JP-00243049.
 XX PR 11-OCT-2001; 2001JP-00344489.
 XX XX (KIRI) KIRIN BEER KK.
 XX PA Mori E, Kataoka S;
 XX PI WPI; 2003-120790/11.
 XX DR N-PSDB; ABZ59698.
 XX XX

XX New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
 XX cells and without exerting an effect on normal cells expressing TRAIL-Rs
 XX nor inducing injury to hepatocytes, for use in therapy of malignant
 XX tumor.
 XX PT
 XX PS Claim 54; Page 62; 92pp; Japanese.

XX The present invention describes antibodies or their functional fragments
 CC that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
 CC have cytostatic and apoptotic activities, and can be used in antibody

CC therapy. The antibodies can be applied as remedies and preventives of
 CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
 CC in the therapy of malignant tumours. Remedies produced with the
 CC antibodies are highly safe, and avoid hepatotoxicity. The present
 CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
 CC present invention
 XX
 SQ Sequence 145 AA;

Query Match 83.1%; Score 558.5; DB 6; Length 145;
 Best Local Similarity 83.3%; Pred. No. 7.3e-44;
 Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;
 QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
 DB 20 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNTDSTGY 79
 QY 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGY-SYNDYYGMDVWGQGT 119
 DB 80 PQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCARSGSGSYRDYYGMDVWGQGT 139
 QY 120 VTVSS 125
 DB 140 VTVSS 145

RESULT 3
 ADA89120
 ID ADA89120 standard; protein; 126 AA.
 XX AC ADA89120;
 XX DT 20-NOV-2003 (first entry)
 XX DE MS-Pro-26-VH amino acid sequence SEQ ID NO:108.
 XX KW antigen binding; antibody; specific binding affinity;
 XX KW receptor protein tyrosine kinase; RPTK;
 XX KW receptor protein tyrosine kinase inhibitor;
 XX KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
 XX KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
 XX KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
 XX KW hypochondroplasia; craniosynostosis disorder;
 XX KW malignant cell proliferative disease; cancer;
 XX KW non-neoplastic angiogenic pathologic condition.

XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO2002102973-A2.
 XX PD 27-DEC-2002.
 XX PF 20-JUN-2002; 2002WO-IL000495.
 XX PR 20-JUN-2001; 2001US-0299187P.
 XX XX (PROC-) PROCHON BIOTECH LTD.
 XX XX Yayon A, Rom E;
 XX XX WPI; 2003-175236/17.
 XX XX

XX New antibodies which have specific binding affinity for a receptor
 XX protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
 XX useful for treating bone and cartilage disorders, or malignant cell
 XX proliferative diseases.
 XX PT
 XX PS Claim 52; Page 19; 122pp; English.

XX The present invention describes a molecule (I) comprising the antigen
 CC binding portion of an isolated antibody which has specific binding
 CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for

CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
CC activation of an RPTK. Also described: (1) pharmaceutical compositions
CC comprising (i) as an active ingredient and a pharmaceutical carrier,
CC reagent for detecting the presence of (i) when bound to the RPTK, and
CC instructions for use; (3) a method for treatment of bone and cartilage
CC related disorders by administering a composition of (1) to the subject;
CC (4) a method for treating or inhibiting a cell proliferative disease or
CC disorder by administering the composition of (1); (5) a method for
CC screening a molecule comprising the antigen-binding portion of an
CC antibody which blocks ligand-dependent activation of RPTK; (6) an
CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region
CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
CC (7); and (9) host cells transformed with the vector. (1) have
CC osteopathic, cytostatic and ophthalmological activities, and can be used
CC as a RPTK inhibitor. Compositions comprising (i) are useful for treating
CC bone and cartilage disorders, including skeletal disorders such as
CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia,
CC hypochondroplasia, severe achondroplasia with developmental delay and
CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
CC nigricans). The composition may also be used for treating or inhibiting
CC malignant cell proliferative disease or disorder associated with abnormal
CC RPTK activity, including a haematopoietic malignancy (e.g. multiple
CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,
CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
CC tumours, tumour progression (particularly progression of transitional
CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the
CC cell proliferative disorder may be associated with the action of a
CC constitutively activated RPTK, or with ligand-dependent activation of
CC RPTK. The compositions may further be used for treating
CC hyperproliferative diseases and disorders associated with ligand-
CC dependent FGFR signaling, such as vision disorders (e.g. neovascular
CC glaucoma, macular degeneration and proliferative retinopathy including
CC diabetic retinopathy), and non-neoplastic angiogenic pathologic
CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
CC invention is given in the exemplification of the present invention.
XX Sequence 126 AA;

Query Match 82.4%; Score 553.5; DB 6; Length 126;
Best Local Similarity 82.9%; Pred No. 1.8e-43;
Matches 107; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNNSGNTNY 60
QY 61 AKKFGRTVTMTDTSISTAYMELSLRSEDIAIYCVKRGFVSY---NYDYVYGMVDVWG 116
Db 61 AKKFGRTVTMTDTSISTAYMELSLRSEDIAIYCVKRGYVAFTYINYGTF---DNWG 117
QY 117 QGTTVTSS 125
Db 118 QGTLVTSS 126

RESULT 4
ADA89122
ID ADA89122 standard; protein; 127 AA.
XX AC ADA89122;
XX DT 20-NOV-2003 (first entry)
XX DE MS-Pro-29-VH amino acid sequence SEQ ID NO:110.
XX KW antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;

KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer; tumour; vision disorder;
XX non-neoplastic angiogenic pathologic condition.
OS Synthetic.
OS Homo sapiens.
XX WO2002102973-A2.
XX 27-DEC-2002.
XX 20-JUN-2002; 2002WO-IL000495.
XX 20-JUN-2001; 2001US-0299187P.
XX (PROC-) PROCHON BIOTECH LTD.
XX Yayan A, Rom E;
XX WPI; 2003-175236/17.
XX New antibodies which have specific binding affinity for a receptor
PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
PT useful for treating bone and cartilage disorders, or malignant cell
PT proliferative diseases.
XX Claim 52; Page 19; 122pp; English.
XX The present invention describes a molecule (I) comprising the antigen
XX binding portion of an isolated antibody which has specific binding
XX affinity for a receptor protein tyrosine kinase (RPTK), particularly for
XX a fibroblast growth factor receptor (FGFR), and which blocks constitutive
XX activation of an RPTK. Also described: (1) pharmaceutical compositions
XX comprising (i) as an active ingredient and a pharmaceutical carrier,
XX reagent for detecting the presence of (i) when bound to the RPTK, and
XX instructions for use; (3) a method for treatment of bone and cartilage
XX related disorders by administering a composition of (1) to the subject;
XX (4) a method for treating or inhibiting a cell proliferative disease or
XX disorder by administering the composition of (1); (5) a method for
XX screening a molecule comprising the antigen-binding portion of an
XX antibody which blocks ligand-dependent activation of RPTK; (6) an
XX isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
XX CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region
XX and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
XX (7); and (9) host cells transformed with the vector. (I) have
XX osteopathic, cytostatic and ophthalmological activities, and can be used
XX as a RPTK inhibitor. Compositions comprising (i) are useful for treating
XX bone and cartilage disorders, including skeletal disorders such as
XX skeletal dysplasia (achondroplasia, thanatophoric dysplasia,
XX hypochondroplasia, severe achondroplasia with developmental delay and
XX acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
XX Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
XX nigricans). The composition may also be used for treating or inhibiting
XX malignant cell proliferative disease or disorder associated with abnormal
XX RPTK activity, including a haematopoietic malignancy (e.g. multiple
XX myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,
XX colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
XX tumours, tumour progression (particularly progression of transitional
XX cell carcinoma or mammary carcinoma), or tumour metastasis, where the
XX cell proliferative disorder may be associated with the action of a
XX constitutively activated RPTK, or with ligand-dependent activation of
XX RPTK. The compositions may further be used for treating
XX hyperproliferative diseases and disorders associated with ligand-
XX dependent FGFR signaling, such as vision disorders (e.g. neovascular
XX glaucoma, macular degeneration and proliferative retinopathy including
XX diabetic retinopathy), and non-neoplastic angiogenic pathologic
XX conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
XX invention is given in the exemplification of the present invention.
XX Sequence 127 AA;

Query Match 82.0%; Score 551; DB 6; Length 127;
 Best Local Similarity 84.3%; Pred. No. 3.1e-43;
 Matches 107; Conservative 6; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWIINPNSGNTDY 60
 Db 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWIINPNSGNTDY 60
 QY 61 AQKFGQGVMTMDTSTISAYMELSLRSEDATLYYCVRGFGY--DYIYGMVDMVWGQ 118
 Db 61 AQKFGQGVMTMDTSTISAYMELSLRSEDATLYYCVRGFGY--DYIYGMVDMVWGQ 118
 QY 119 TITVTSS 125
 Db 121 TLTVTSS 127

RESULT 5
 ADA89202
 ID ADA89202 standard; protein; 128 AA.
 XX ADA89202;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.
 XX
 KW immunoglobulin; Ig; heavy chain variable domain;
 KW light chain variable domain; major histocompatibility complex; MHC;
 KW Sp100; MUC1; TAX; hTERT; cytosolic; gene therapy; cancerous disorder;
 KW cancer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070752-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-FEB-2003; 2003WO-US005128.
 XX
 PR 20-FEB-2002; 2002US-0358994P.
 XX
 XX (DYAX-) DYAX CORP.
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Hoogenboom HRJM, Reiter Y;
 XX
 DR WPI; 2003-663847/62.
 DR N-PSDB; ADA89201.
 XX
 PT New protein comprising an immunoglobulin heavy chain variable (VH) domain
 PT and an immunoglobulin light chain variable (VL) domain, useful for
 PT preparing a composition for treating or preventing a cancerous disorder.
 XX
 PS Disclosure; Fig 10B; 224pp; English.
 XX
 CC The present invention describes a protein comprising an immunoglobulin
 CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
 CC domain. The protein binds a complex comprising a major histocompatibility
 CC complex (MHC) and a peptide, does not substantially bind the MHC in the
 CC absence of the bound peptide, and does not substantially bind the peptide
 CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
 CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
 CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
 CC comprising one or more nucleic acids for expressing the Ig that binds a
 CC complex having an MHC and a peptide, does not substantially bind the MHC
 CC in the absence of the bound peptide, and does not substantially bind the MHC
 CC peptide in the absence of the MHC; (3) an isolated nucleic acid
 CC comprising a first segment that encodes the Ig variable domain; (4) a
 CC host cell comprising heterologous nucleic acid sequences that encodes the
 CC novel protein; (5) a transgenic animal whose genome includes heterologous
 CC nucleic acid sequences that encode the protein; (6) identifying the

CC protein that specifically binds the MHC-peptide complex; (7) expressing
 CC an antigen-binding protein; (8) ablating or killing a target cell that
 CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents the heavy chain of an antibody which binds to an MHC-
 CC peptide complex where the peptide component in as peptide fragment of
 CC gp100.
 SQ Sequence 128 AA;

Query Match 81.5%; Score 547.5; DB 6; Length 128;
 Best Local Similarity 83.6%; Pred. No. 6.6e-43;
 Matches 107; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWIINPNSGNTDY 60
 Db 1 EVQLVQSGAEVKKPKGASVKVSKASGYTFTSYIHWRQAPGQGLEWGMGAINPSSGSTPY 60
 QY 61 AQKFGQGVMTMDTSTISAYMELSLRSEDATLYYCVRGFGY--SYNDYIYGMVDMVWGQ 117
 Db 61 AQKFGQGVMTMDTSTISAYMELSLRSEDATLYYCVRGFGY--SYNDYIYGMVDMVWGQ 120
 QY 118 GTTIVTSS 125
 Db 121 GTTIVTSS 128

RESULT 6
 AAW88464
 ID AAW88464 standard; protein; 476 AA.
 XX AAW88464;
 AC AAW88464;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Monoclonal antibody 4B5 heavy chain variable region.
 XX
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm;
 KW diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma;
 KW lung carcinoma; metastasis; anti-idiotypic antibody; GD2 antigen; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9902545-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 08-JUL-1998; 98WO-IB001046.
 XX
 PR 08-JUL-1997; 97US-0051945P.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Dan MD;
 XX
 DR WPI; 1999-120769/10.
 DR N-PSDB; AAX06951.
 XX
 PT New antibody 4B5 polynucleotides and polypeptides - used to develop
 PT products for the diagnosis and treatment of cancers and for prophylactic
 PT therapy to reduce risk of recurrence.
 XX
 PS Claim 1; Page 79-80; 83pp; English.
 XX
 CC This polypeptide comprises the heavy chain variable region of the
 CC recombinant human monoclonal antibody (MAB) 4B5. 4B5 recognises
 CC antibodies specific for GD2 antigen antibodies. Antibodies specific for
 CC GD2 recognise various cancers including glioblastoma, neuroblastoma,
 CC malignant and/or metastatic melanoma, breast adenocarcinoma, lung
 CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and

CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with
 CC immunologic specificity for antibodies specific for GD2. These
 CC derivatives, or antigen binding fragments, comprise regions of the 4B5
 CC VDJ junction and regions spanning the 4B5 CDRs. Other derivatives include
 CC Fab, F(ab')₂, Fab', scFv and isolated heavy and light chains (see also
 CC AAW88465). Polynucleotide fragments (see AAX06951-54) encoding 4B5
 CC antibody V regions are also provided, and therapeutic plasmids and
 CC vectors, including vaccinia virus vectors, comprising these
 CC polynucleotides. 4B5 has been shown to mimic GD2, and is particularly
 CC useful in generating a host immune response to cancer. Products of the
 CC invention can be used in the detection and treatment of e.g. astrocytoma,
 CC oligodendroglioma, spindleoma, medulloblastoma, primitive neural
 CC ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and
 CC large cell lung adenocarcinomas, squamous cell carcinoma,
 CC bronchoalveolar carcinoma, epithelial adenocarcinoma, and liver metastases,
 CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular
 CC adenocarcinoma, squamous and adenocarcinomas of the uterine cervix,
 CC uterine and ovarian epithelial carcinoma, prostatic adenocarcinoma,
 CC transitional squamous cell carcinoma of the bladder, B and T cell
 CC lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
 CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma
 XX

Sequence 476 AA;

Query Match 81.0%; Score 544; DB 2; Length 476;
 Best Local Similarity 78.9%; Pred. No. 5.8e-42;
 Matches 105; Conservative 7; Mismatches 7; Indels 14; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSVDINWVQATGCGLEWGWNPNSGNTDY 60
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSVDLNVWVQAPQGQLEWGWNPNSGKTGY 79
 QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYCYVRGFGYSVNYD-----YYGGM 112
 DB 80 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYFCAR-----NADNVMAAIYHYGGM 133
 QY 113 DWVGQGTVTTVSS 125
 DB 134 DWVGQGTVTTVSS 146

RESULT 7

ADA89116
 ID ADA89116 standard; protein; 126 AA.
 XX
 AC ADA89116;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE MS-Pro-11-VH amino acid sequence SEQ ID NO:104.
 XX
 KW antigen binding; antibody; specific binding affinity;
 KW receptor protein tyrosine kinase; RPTK;
 KW receptor protein tyrosine kinase inhibitor;
 KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
 KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
 KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
 KW hypochondroplasia; craniosynostosis disorder;
 KW malignant cell proliferative disease; cancer; tumour; vision disorder;
 KW non-neoplastic angiogenic pathologic condition.

Synthetic.

Homo sapiens.

W02002102973-A2.

27-DEC-2002.

20-JUN-2002; 2002WO-IL000495.

20-JUN-2001; 2001US-0299187P.

(PROC-) PROCHON BIOTECH LTD.

XX

PI Yayon A, Rom E;

XX WPI; 2003-175236/17.

XX New antibodies which have specific binding affinity for a receptor
 PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
 PT useful for treating bone and cartilage disorders, or malignant cell
 PT proliferative diseases.

XX Claim 52; Page 18; 122pp; English.

XX The present invention describes a molecule (I) comprising the antigen
 CC binding portion of an isolated antibody which has specific binding
 CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for
 CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
 CC activation of an RPTK. Also described: (1) pharmaceutical compositions
 CC comprising (I) as an active ingredient and a pharmaceutical carrier,
 CC excipient, or auxiliary agent; (2) a kit comprising (I), at least one
 CC reagent for detecting the presence of (I) when bound to the RPTK, and
 CC instructions for use; (3) a method for treatment of bone and cartilage
 CC related disorders by administering a composition of (I) to the subject;
 CC (4) a method for treating or inhibiting a cell proliferative disease or
 CC disorder by administering the composition of (I); (5) a method for
 CC screening a molecule comprising the antigen-binding portion of an
 CC antibody which blocks ligand-dependent activation of RPTK; (6) an
 CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
 CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VI region
 CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
 CC (7); and (9) host cells transformed with the vector. (I) have
 CC osteopathic, cytostatic and ophthalmological activities, and can be used
 CC as a RPTK inhibitor. Compositions comprising (I) are useful for treating
 CC bone and cartilage disorders, including skeletal disorders such as
 CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia, and
 CC hypochondroplasia, severe achondroplasia with developmental delay and
 CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
 CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
 CC nigricans). The composition may also be used for treating or inhibiting
 CC malignant cell proliferative disease or disorder associated with abnormal
 CC RPTK activity, including a haematopoietic malignancy (e.g. multiple
 CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, and
 CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
 CC tumours, tumour progression (particularly progression of transitional
 CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the
 CC cell proliferative disorder may be associated with the action of a
 CC constitutively activated RPTK, or with ligand-dependent activation of
 CC RPTK. The compositions may further be used for treating
 CC hyperproliferative diseases and disorders associated with ligand-
 CC dependent FGFR signaling, such as vision disorders (e.g. neovascular
 CC glaucoma, macular degeneration and proliferative retinopathy including
 CC diabetic retinopathy), and non-neoplastic angiogenic pathologic
 CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present
 CC sequence is given in the exemplification of the present invention.

Sequence 126 AA;

Query Match 80.7%; Score 542.5; DB 6; Length 126;
 Best Local Similarity 83.5%; Pred. No. 1.9e-42;
 Matches 106; Conservative 7; Mismatches 11; Indels 3; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSVDINWVQATGCGLEWGWNPNSGNTDY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNHWVWVQAPQGQLEWGWNPNSGNTNY 60
 QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYCYVRGFGYSVNYDYYG--MDVWGQG 118
 DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYCYARYGSSL-YHYVFGGFDYWGQG 119
 QY 119 TTVTVSS 125
 DB 120 TLTVTSS 126

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RESULT 8
AAW27551
ID AAW27551 standard; protein; 120 AA.
XX AC AAW27551;
XX DT 23-JAN-1998 (first entry)
XX DE Human Ab heavy chain variable region VH1B consensus.
XX KW Human; antibody; preparation; library; VH1B; variable region;
XX KW heavy chain; consensus.
XX OS Homo sapiens.
XX PN WC9708320-A1.
XX XX
XX PD 06-MAR-1997.
XX PF 19-AUG-1996; 96WO-EP003647.
XX PR 18-AUG-1995; 95EP-00113021.
XX PA (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MSH.
XX FI Knappik A, Pack P, Ilag V, Ge L, Moroney S, Plueckthun A;
XX DR WPI; 1997-179277/16.
XX DR N-PSDB; AAT87949.
XX PT Preparation of human derived antibody gene library - using synthetic
XX PT consensus sequences, and signal consensus antibody gene as universal
XX PT framework for highly diverse antibody libraries.
XX PS Example 1; Fig 5B; 436pp; English.
XX CC The present sequence is the human antibody heavy chain variable region
XX CC synthetic sequence VH1B, used in the preparation of a human derived
XX CC antibody gene library
XX SQ Sequence 120 AA;

Query Match 80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 2.2e-42;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQAPQGQLEWMGWINPNSGGTNY 60
Qy 61 AQKFGQRTVTRDTSTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVTRDTSTAYMELSLRSEDTAIYYCARWGG-----DGFYAMDYWGQGT 115
Qy 121 VTVSS 125
Db 116 VTVSS 120

RESULT 9
AAW22841
ID AAW22841 standard; protein; 146 AA.
XX AC AAW22841;
XX DT 12-SEP-1997 (first entry)
XX DE Human anti-tumour antigen antibody heavy chain variable region.
XX KW Human; tumour antigen; cancer; monoclonal; antibody; heavy chain;
XX KW variable region; medicine; pharmacology; biochemistry; CDR;
XX KW complementarity determining region.
XX XX

RESULT 10
ADD28330
ID ADD28330 standard; protein; 136 AA.
XX AC ADD28330;
XX DT 15-JAN-2004 (first entry)
XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:108.
XX KW human heterodimeric antibody; human; antibody; binding affinity;
XX KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
XX KW edema factor; lethal factor; viricide; antibacterial; immunotherapy;
XX KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX XX

OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..146
FT Region /label= mat_peptide
FT Region 50..54
FT Region /label= CDR_1
FT Region 69..85
FT Region /label= CDR_2
FT Region 118..139
FT Region /label= CDR_3
XX JF09100300-A.
XX PD 15-APR-1997.
XX PF 03-OCT-1995; 95JP-00278266.
XX PR 03-OCT-1995; 95JP-00278266.
XX PA (HAGI/) HAGIWARA Y.
XX DR WPI; 1997-276726/25.
XX DR N-PSDB; AAT75422.
XX PT Anticancer human monoclonal antibody variable region sequences - and
XX PT related DNA and RNA.
XX PS Claim 3; Page 10; 14pp; Japanese.
XX CC The present sequence is a human anti-tumour antigen monoclonal antibody
XX CC (MAB) heavy chain variable region, useful in medicine, pharmacology and
XX CC biochemistry. The isotype of a MAB secreted by the human/human hybridoma
XX CC HT was determined to be mu and kappa. Human MAB was purified, and the
XX CC antigen recognised by human MAB CLN"-IgM identified by western blotting
XX SQ Sequence 146 AA;

Query Match 80.5%; Score 541; DB 2; Length 146;
Best Local Similarity 83.5%; Pred. No. 3e-42;
Matches 106; Conservative 6; Mismatches 9; Indels 6; Gaps 3;

Qy 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQAPQGQLEWMGWINPNSGGTNY 79
Qy 61 AQKFGQRTVTRDTSTAYMELSLRSEDTAIYYCVRG-FGY-----SYND-YYYGMDV 114
Db 80 AQKFGQRTVTRDTSTAYMELSLRSEDTAIYYCVRG-FGY-----SYND-YYYGMDV 139
Qy 115 WQGGTTV 121
Db 140 WQGGTTV 146

RESULT 10
ADD28330
ID ADD28330 standard; protein; 136 AA.
XX AC ADD28330;
XX DT 15-JAN-2004 (first entry)
XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:108.
XX KW human heterodimeric antibody; human; antibody; binding affinity;
XX KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
XX KW edema factor; lethal factor; viricide; antibacterial; immunotherapy;
XX KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX XX

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OS Synthetic.
OS Homo sapiens.
XX WO2003076568-A2.
XX
XX 18-SEP-2003.
XX
XX 11-FEB-2003; 2003WO-US004206.
XX
XX 11-FEB-2002; 2002US-0356086P.
PR 29-APR-2002; 2002US-0376408P.
PR 27-SEP-2002; 2002US-0414053P.
PR 25-NOV-2002; 2002US-0428807P.
XX
XX (ALEX-) ALEXION PHARM INC.
XX
XX Bowdish KS, Wild WA;
XX WPI; 2003-722327/68.
XX
XX New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
XX Claim 11; SEQ ID NO 108; 67pp; English.
XX
XX The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
XX Sequence 136 AA;
SQ
Query Match 80.1%; Score 538; DB 7; Length 136;
Best Local Similarity 80.0%; Pred. No. 5.3e-42;
Matches 104; Conservative 7; Mismatches 13; Indels 6; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60
DB 3 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGWINPNTGNTNY 62
QY 61 AQKFGQVYTMRTDTSISTAYMELSLRSEDTAIYCVRGF-----GYSYNDYVYGMGVW 115
DB 63 AQNFGQVYTMRTDTSIRIAYTELRLRLRSDDTAVYICARDFYSDSSGYIYGY-YSYGMGVW 121
QY 116 GQGTITVTSS 125
DB 122 GQGTITVTSS 131
RESULT 11
AA34301
ID AA34301 standard; protein; 203 AA.
XX
XX AA34301;
AC
DT 19-NOV-1999 (first entry)
XX
XX IgM antibody CEM 10.12 F3 heavy chain sequence.
DE
XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.
XX WO9945031-A2.
XX
XX 10-SEP-1999.
XX
XX 03-MAR-1999; 99WO-US004583.
XX
XX 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Davis CG, Blacher RW, Corvaian JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
XX WPI; 1999-540816/45.
DR N-PSDB; AA220402.
XX
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
PT
XX
XX Claim 60; Fig 26; 245pp; English.
XX
XX This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
XX Sequence 203 AA;
SQ
Query Match 79.9%; Score 537; DB 2; Length 203;
Best Local Similarity 89.7%; Pred. No. 1e-41;
Matches 102; Conservative 5; Mismatches 6; Indels 2; Gaps 2;
QY 12 KKPASVKVSKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDYAQKFGQVYTM 71
DB 1 KKPASVKVSKASGYTFTSYDINVRQATGQGLEWMGWINPNSGNTGYAQKFGQVYTM 60
QY 72 RDTSTSTAYMELSLRSEDTAIYCVRGFYSYNDY-YVGMGVGQGTITVTSS 125
DB 61 RNTSISTAYMELSLRSEDTAIYCVRGF-HGGSYFYIYGMGVGQGTITVTSS 114
RESULT 12
ADA89123
ID ADA89123 standard; protein; 126 AA.
XX
XX ADA89123;
AC
DT 20-NOV-2003 (first entry)
XX
XX MS-Pro-54-VH amino acid sequence SEQ ID NO:111.
DE
XX antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer;
XX non-neoplastic angiogenic pathologic condition.
XX
XX Synthetic.

CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a heavy chain variable region of an anti-Ang-2
CC antibody
XX
SQ Sequence 125 AA;

Query Match 79.8%; Score 536; DB 6; Length 125;
Best Local Similarity 81.8%; Pred. No. 7.4e-42;
Matches 102; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKPGASVKVSKCASKGYTFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVOLVSGAEVKPGASVKVSKCASKGYTFTSYGIVSRQAPGQGLEWMGWISAYNGTNY 60

QY 61 AQKQGRVMTTRDTSTSTAYMELSLRSRSDTAIYVCVGFSGYSNYDYIYGMVWGQGT 120
DB 61 AQKQGRVMTTRDTSTSTAYMELSLRSRSDTAIYVCVGFSGYSNYDYIYGMVWGQGT 120

QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 15
ADA89115
ID ADA89115 standard; protein; 118 AA.
XX
AC ADA89115;
XX
DT 20-NOV-2003 (first entry)
XX
XX MS-Pro-2-VH amino acid sequence SEQ ID NO:103.
DE
XX antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer; tumour; vision disorder;
XX non-neoplastic angiogenic pathologic condition.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WC02002102973-A2.
XX
PD 27-DEC-2002.
XX
XX 20-JUN-2002; 2002WO-IL000495.
PF
XX 20-JUN-2001; 2001US-0299187P.
PR
XX (PROC-) PROCHON BIOTECH LTD.
PA
XX Yayon A, Rom E;
PI
XX WPI; 2003-175236/17.
DR
XX New antibodies which have specific binding affinity for a receptor
PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
PT useful for treating bone and cartilage disorders, or malignant cell
PT proliferative diseases.
XX
XX Claim 42; Page 18; 122pp; English.
XX

The present invention describes a molecule (I) comprising the antigen
CC binding portion of an isolated antibody which has specific binding
CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for
CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
CC activation of an RPTK. Also described: (i) pharmaceutical compositions
CC comprising (I) as an active ingredient and a pharmaceutical carrier,
CC

Query Match	79.8%;	Score 536.5;	DB 5;	Length 247;	
Best Local Similarity	81.6%;	Pred. No. 1.4e-41;			
Matches 102;	Conservative	8;	Mismatches 14;	Indels 1;	Gaps 1;
QY	1	QVQLVQSGAEVKKPKASVKVCKASGVTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY	60		
Db	1	QVQLVQSGAEVKKPKASVKVCKASGVTFTSYDINWVRQAPGQGLEWGWGWINPNSGNTNY	60		
QY	61	AKQFQGRVTMTDTSISAYMELSLKRSDDTAIVYCVRGFGYSVNDYVYGVMDVWGSGTT	120		
Db	61	AKQFQGRVTMTDTSISAYMELSLKRSDDTAIVYCVRGFGYSVNDYVYGVMDVWGSGTT	120		
QY	121	VTVSS 125			
Db	120	VTVSS 124			
RESULT 14					
ABR55813					
ID	ABR55813	standard; protein; 125 AA.			
XX					
XX	ABR55813;				
XX					
DT	02-SEP-2003	(first entry)			
DE		Heavy chain variable region of anti-Ang-2 antibody FJ-G11 HC.			
XX					
KW	Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;				
KW	gynaecological; antiinflammatory; osteopathic; antipsozotic; cancer;				
KW	angiogenesis; antibody.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	Region	26..36			
FT	Region	/notes="complementarity determining region (CDR) 1"			
FT	Region	50..66			
FT	Region	/notes="complementarity determining region (CDR) 2"			
FT	Region	96..115			
FT	Region	/notes="complementarity determining region (CDR) 3"			
XX					
FN	WC0203030833-A2.				
XX					
PD	17-APR-2003.				
XX					
PF	11-OCT-2002;	2002WO-US032613.			
XX					
PR	11-OCT-2001;	2001US-0328604P.			
PR	10-OCT-2002;	2002US-00269805.			
XX					
PA	(AMGE-) AMGEN INC.				
XX					
FI	Oliner JD;				
XX					
DR	WPI; 2003-504963/47.				
XX					
PT	New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful				
PT	for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,				
PT	hemangioma, arteriosclerosis, atherosclerosis or endometriosis.				
XX					
PS	Claim 1; Page 92; 161pp; English.				
XX					
CC	The invention relates to a specific binding agent, which comprises at				
CC	least one peptide selected from any of 62 peptides (ABR55769-930) or its				
CC	fragment. The binding agents are antibodies that recognize and bind to				
CC	angiotensin-2 (Ang-2). The specific binding agent, particularly the				
CC	antibody, is useful for inhibiting undesired angiogenesis, treating				
CC	cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-				
CC	2 activity, modulating vascular permeability or plasma leakage, or				
CC	treating a disease (e.g. ocular neovascular disease, obesity,				
CC	haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,				
CC	inflammatory disorders, atherosclerosis, endometriosis, neoplastic				

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:03:52 ; Search time 41.309 Seconds
(without alignments)
836.607 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVOLVSGAEVKPGASVKV.....YDYVGMVWGQTTVTSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	672	100.0	125	14	US-10-041-860-48
2	672	100.0	125	14	US-10-041-860-48
3	672	100.0	125	14	US-10-041-860-237
4	672	100.0	125	14	US-10-041-860-372
5	638	94.9	125	14	US-10-041-860-38
6	638	94.9	125	14	US-10-041-860-203
7	638	94.9	125	14	US-10-041-860-240
8	638	94.9	125	14	US-10-041-860-343
9	593.5	88.3	126	14	US-10-041-860-19
10	593.5	88.3	126	14	US-10-041-860-201
11	593.5	88.3	126	14	US-10-041-860-288
12	579.5	86.2	125	14	US-10-041-860-238
13	575.5	85.6	126	14	US-10-041-860-40
14	575.5	85.6	126	14	US-10-041-860-204
15	575.5	85.6	126	14	US-10-041-860-241

16	575.5	85.6	126	14	US-10-041-860-349
17	572	85.1	127	14	US-10-041-860-44
18	572	85.1	127	14	US-10-041-860-205
19	572	85.1	127	14	US-10-041-860-242
20	572	85.1	127	14	US-10-041-860-360
21	567.5	84.4	126	14	US-10-041-860-21
22	567.5	84.4	126	14	US-10-041-860-199
23	567.5	84.4	126	14	US-10-041-860-236
24	567.5	84.4	126	14	US-10-041-860-294
25	562.5	83.7	124	15	US-10-309-762-125
26	561.5	83.6	122	14	US-10-269-805-61
27	561.5	83.6	126	14	US-10-041-860-37
28	561.5	83.6	126	14	US-10-041-860-202
29	561.5	83.6	126	14	US-10-041-860-239
30	551.5	82.1	118	15	US-10-309-762-124
31	547.5	81.5	128	12	US-10-371-942-46
32	544	81.0	476	9	US-09-747-659-3
33	544	81.0	476	14	US-10-250-703-3
34	538	80.1	136	15	US-10-364-743-108
35	536.5	79.8	247	10	US-09-880-748-1729
36	536.5	79.8	247	12	US-10-293-418-1729
37	536	79.8	125	14	US-10-269-805-45
38	534.5	79.5	249	10	US-09-880-748-919
39	534.5	79.5	249	12	US-10-293-418-919
40	529.5	78.8	120	14	US-10-125-687-2
41	528	78.6	127	14	US-10-041-860-31
42	528	78.6	127	14	US-10-041-860-243
43	528	78.6	127	14	US-10-041-860-325
44	527.5	78.5	122	12	US-10-292-088-110
45	527.5	78.5	146	9	US-09-925-299-1050

ALIGNMENTS

RESULT 1

US-10-041-860-48
; Sequence 48, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-48

Query Match 100.0%; Score 672; DB 14; Length 125;

Best Local Similarity 100.0%; Pred. No. 1e-56;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVOLVSGAEVKPGASVKVSKASGYFTSYDINWVRQATCGGLEWGWINPNSGNTDY	60
Db	1	QVOLVSGAEVKPGASVKVSKASGYFTSYDINWVRQATCGGLEWGWINPNSGNTDY	60
Qy	61	AQKFGQVMTTRDTSISTAYMELSSLRSDTAIYCVRGFGYSYNYDYGMVWGQGT	120
Db	61	AQKFGQVMTTRDTSISTAYMELSSLRSDTAIYCVRGFGYSYNYDYGMVWGQGT	120

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Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 2
US-10-041-860-200
; Sequence 200, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-200

Query Match 100.0%; Score 672; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSNYDYGGMDVWGQGT 120
Db 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSNYDYGGMDVWGQGT 120

Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 4
US-10-041-860-372
; Sequence 372, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372

Query Match 100.0%; Score 672; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSNYDYGGMDVWGQGT 120
Db 61 AQKFGQRTVMTDRDTSISTAYMELSLRSEDTAIYYCVRGFGYSNYDYGGMDVWGQGT 120

Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 5
US-10-041-860-38
; Sequence 38, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard

```

```

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-38

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNFNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNFNSGNTGY 60
Qy 61 AQKFGQGVVTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Db 61 AQKFGQGVVTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 6
US-10-041-860-203
; Sequence 203, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-203

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNFNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNFNSGNTGY 60
Qy 61 AQKFGQGVVTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Db 61 AQKFGQGVVTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 7
US-10-041-860-240
; Sequence 240, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-240

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNFNSGNTDY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNFNSGNTGY 60
Qy 61 AQKFGQGVVTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Db 61 AQKFGQGVVTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGIT 120
Qy 121 VTSS 125
Db 121 VTSS 125

RESULT 8
US-10-041-860-343
; Sequence 343, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343

Query Match          94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
QY 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVR-
DB 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAVYICAREGIAVAGTYYYYYGMVWGQGT 120
QY 121 TVTVSS 125
DB 121 TVTVSS 125

RESULT 9
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match 88.3%; Score 593.5; DB 14; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.4e-49;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
QY 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVR-
DB 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAVYICAREGIAVAGTYYYYYGMVWGQGT 119
QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 10
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 88.3%; Score 593.5; DB 14; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.4e-49;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
QY 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVR-
DB 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAVYICAREGIAVAGTYYYYYGMVWGQGT 119
QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 11
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match 88.3%; Score 593.5; DB 14; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.4e-49;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
QY 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVR-
DB 61 AOKFQGRVTMTSDTSISTAYMELSSLRSEDTAVYICAREGIAVAGTYYYYYGMVWGQGT 119
QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 12
US-10-041-860-238
; Sequence 238, Application US/10041860

```

; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match      86.2%; Score 579.5; DB 14; Length 125;
Best Local Similarity 89.4%; Pred. No. 7.3e-48;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQK 63
DB 3 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQK 62

QY 64 FQGRVTMTRTSISTAYMELSLRSEDATAYCYVR-GFGYSYNDYVYGGMDVWGQGT 122
DB 63 FQGRVTMTRTSISTAYMELSLRSEDATAYCYVRGAGTGGTGGTGGTGGTGGTGGT 122

QY 123 VSS 125
DB 123 VSS 125

RESULT 13
US-10-041-860-40
; Sequence 40, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-40

Query Match      85.6%; Score 575.5; DB 14; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.8e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVOLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVOLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTRTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 119
DB 61 AQKFGQGRVTMTRTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 14
US-10-041-860-204
; Sequence 204, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-204

Query Match      85.6%; Score 575.5; DB 14; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.8e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVOLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVOLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTRTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 119
DB 61 AQKFGQGRVTMTRTSISTAYMELSLRSEDATAYCYVRGFGYSYN-YDYVYGGMDVWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 15
US-10-041-860-241
; Sequence 241, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-40

Query Match      85.6%; Score 575.5; DB 14; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.8e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVOLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVOLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

```

```
; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-241

Query Match      85.6%; Score 575.5; DB 14; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.8e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKYSCKASGYTFSTYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKYSCKASGYTFSTYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy 61 AOKFQGRVTMTNRTSISTAYMELSLRSEDTAIYYCVRGFGYSYN-YDYIYGGNDVWGQGT 119
Db 61 AOKFQGRVTMTNRTSISTAYMELSLRSEDTAIYYCVRGFGYSYN-YDYIYGGNDVWGQGT 120

Qy 120 TVTVSS 125
Db 121 TVTVSS 126
```

Search completed: April 21, 2004, 17:13:22
Job time : 42.309 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 38.0901 Seconds
(without alignments)
1035.433 Million cell updates/sec

Title: US-10-041-860-48

Perfect score:

Sequence: 1 QVQLVQSGAEVKKPGASVK...YDYYGMDVWGQGT^TTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs. 315518202 residues

Total number of hits satisfying chosen parameters:	1017041
----------------------------------------------------	---------

Minimum DB seq length: 0

Minimum	DB seq	length:
Maximum	DB seq	length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10

Maximum Match 100%
Listing first 45 summaries

Database :

```

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	497.5	74.0	159	4	Q96QSO	Q96QSO homo sapien
2	494	73.5	119	4	Q9U194	Q9U194 homo sapien
3	494	73.5	125	4	Q9UL95	Q9UL95 homo sapien
4	481.5	71.7	124	4	Q9UL92	Q9UL92 homo sapien
5	474	70.5	497	4	Q8WY24	Q8WY24 homo sapien
6	470.5	70.0	500	4	Q9BRV0	Q9BRV0 homo sapien
7	468	69.6	614	4	Q96GA6	Q96GA6 homo sapien
8	455	67.7	119	5	Q9GVZ2	Q9GVZ2 schistosoma
9	433.5	64.5	469	4	Q7Z7P5	Q7Z7P5 homo sapien
10	431.5	64.2	278	11	Q921K1	Q921K1 mus musculu
11	430	64.0	481	11	Q91W11	Q91W11 mus musculu
12	429.5	63.9	116	4	Q9UL89	Q9UL89 homo sapien
13	425.5	63.3	145	11	Q924R4	Q924R4 mus musculu
14	422	62.8	147	11	Q925S3	Q925S3 mus musculu
15	420	62.5	157	4	Q95978	Q95978 homo sapien
16	419	62.4	470	11	Q7TMK1	Q7TMK1 mus musculu

ALIGNMENTS

RESULT 1

Q96QSO
TO Q96QSO
PRELIMINARY:
PRT: 159 AA.

AD	Q96QSU	FREEMANNAI; FR;
ID	Q96QSU;	
AC	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Putative matrix cell adhesion molecule-3.	
DE	Homo sapiens (Human).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]_SEQUENCE FROM N.A.	
RP		

Query Match	74.0%;	Score 497.5;	DB 4;	Length 159;
Best Local Similarity	74.0%;	Pred. No. 1.2e-42;		
Matches	97;	Conservative	12;	Mismatches 15;
				Indels 7

Qy	1	QVQLVQSGAEVKPKGASVKYSCKASGYFTFSYDINNVROATGGCLFWMGWHPNSGNTDY	60
		: :: :	
Db	20	QVQLVQSGAEVKPKGASVKYSCKASGYFTSYNNVVRRAPGGPEWMMGVNPSGGSARY	79
		: :: :	
Qy	61	AQKFGGRVTITRDTSTISAYNELSSLSSEPTAIYCVR-----GFQSYNYDIYYIGMDV	114
		: :: :	
Db	80	SKQFQGLRTITRDTSTSTVYNDLSRLSDDDTAVYFCAREMEITFGGAIVSKGP-YYYIGMDV	138
		: :: :	
Qy	115	WGQGTTTVTVSS	125

```
Db 139 WGQGTVTVSS 149
|||||
RESULT 2
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94; 2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 73.5%; Score 494; DB 4; Length 119;
Best Local Similarity 76.0%; Pred. No. 2e-42;
Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYVHWVRQAPGQGLEWGWGWINPNSWTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGGGLWF-----DPWGQGT 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VTVSS 125
Db 115 VTVSS 119

RESULT 3
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95; 2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 71.7%; Score 481.5; DB 4; Length 124;
Best Local Similarity 76.0%; Pred. No. 3.8e-41;
Matches 95; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTSYVHWVRQAPGQGLEWGWGWINPNSGTSY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGL-YVVPAPAFSRFDYWGQGT 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C32488EAC CRC64;

Query Match 73.5%; Score 494; DB 4; Length 125;
Best Local Similarity 76.0%; Pred. No. 2.1e-42;
Matches 95; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYVHWVRQAPGQGLEWGWGWINPNSGGTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGGGLR-AAAAGDAPDIMGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VTVSS 125
Db 121 VTVSS 125

RESULT 4
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92; 2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 71.7%; Score 481.5; DB 4; Length 124;
Best Local Similarity 76.0%; Pred. No. 3.8e-41;
Matches 95; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTSYVHWVRQAPGQGLEWGWGWINPNSGTSY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGMVWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGQRTVTRDTSISTAYMELSLRSDDTAVYYCARGL-YVVPAPAFSRFDYWGQGT 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 121 VTSS 125
Db 120 VTSS 124

RESULT 5
Q8WY24
ID Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SMC66, a Ig-like gene which is
RT down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283656; AAL36987.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 5365 MW; F24D08DFA5A63E5 CRC64;

Query Match 70.5%; Score 474; DB 4; Length 497;
Best Local Similarity 70.0%; Pred. No. 1.2e-39;
Matches 91; Conservative 13; Mismatches 16; Indels 10; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGWINPNSGNTDY 60
Db 20 QEQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGWINPNSGNTDY 79

QY 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGF-GYS--YNYDYIYGMVDVW 115
Db 80 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGF-GYS--YNYDYIYGMVDVW 134

QY 116 GQGTIVTVSS 125
Db 135 GQGTIVTVSS 144

RESULT 6
Q8WY24
ID Q8WY24 PRELIMINARY; PRT; 500 AA.
AC Q8WY24
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1;
DR HSSP; P01789; LMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 4.

Query Match 69.6%; Score 468; DB 4; Length 614;
Best Local Similarity 73.6%; Pred. No. 6.4e-39;
Matches 92; Conservative 14; Mismatches 15; Indels 4; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGWINPNSGNTDY 60
Db 20 QMQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGWITPFNGNTNY 79

QY 61 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGF-GYS--YNYDYIYGMVDVW 120
Db 80 AQKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGF-GYS--YNYDYIYGMVDVW 135

QY 121 VTSS 125
Db 136 VTSS 140
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RESULT 8
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.I., feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2F84
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 67.7%; Score 455; DB 5; Length 119;
Best Local Similarity 69.6%; Pred. No. 1.8e-38;
Matches 87; Conservative 14; Mismatches 18; Indels 6; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNSGNTDY 60
DB 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQAPGHLGIEWGINPSGYTNY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQTT 120
DB 61 NQKFKDRVTMTDKSFSTAYMDLSRLSADSAVYYCAR-----YDDHYCLDYWGQGT 114
QY 121 VTVSS 125
DB 115 VTVSS 119

RESULT 9
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=Splice;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C8D5B5E12BAAF795C CRC64;

Query Match 64.5%; Score 433.5; DB 4; Length 469;
Best Local Similarity 66.4%; Pred. No. 1.5e-35;
Matches 85; Conservative 13; Mismatches 19; Indels 11; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNSGNTDY 60
DB 20 QVHLVSGAEVKKPGASVKLSCKTSYNTFSYDILWVRQAPGQGLEWGMWISAHNGDTKY 79
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQ 117
DB 80 ARKFGQRTVTRDTSATTSMYEFRLSRDSDTALFYCATKSRG-----QVGFDFSWGQ 131
QY 118 GTTVVSS 125
DB 132 GTLVVSS 139

RESULT 10
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 64.2%; Score 431.5; DB 11; Length 278;
Best Local Similarity 66.4%; Pred. No. 1.2e-35;
Matches 83; Conservative 16; Mismatches 21; Indels 5; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNSGNTDY 60
DB 20 QVQLVSGAEVKKPGASVKLSCKASGYTFTSYMHWVQKRRGQGLEWGINPNSGNTNY 79
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDTAIYVCV---RGFGSYNYDYIGMDVWGQTT 120
DB 80 ARKFGQRTVTRDTSATTSMYEFRLSRDSDTALFYCATKSRG-----QVGFDFSWGQ 131
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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 1.  
FT NON_TER 145  
SQ SEQUENCE 145 AA; 16081 MW; ECDLIAI35E05B8AA CRC64;  
  
Query Match 63.3%; Score 425.5; DB 11; Length 145;  
Best Local Similarity 64.8%; Pred. No. 2.2e-35;  
Matches 81; Conservative 17; Mismatches 22; Indels 5; Gaps 1;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
Db 1 QVQLQPGAEVKKPGASVKLSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
Qy 61 AQKFGQRTVMTDRTSISTAYMELSLRSEDTAIYVCVRFSGYSYNDYYGMDVWGQGT 120  
Db 61 NEKPKSKATLTVDPSSATAYMQLSLTSDSAVYICARS-----DYDYDYAMDYWGQGT 115  
  
Qy 121 TVTVSS 125  
Db 116 TVTVSS 120  
  
RESULT 14  
Q925S3 PRELIMINARY; PRT; 147 AA.  
AC Q925S3 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE MRP3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice."  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RA "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain."  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240166; AAK43731.1; --  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 1.  
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;  
  
Query Match 62.8%; Score 422; DB 11; Length 147;  
Best Local Similarity 65.1%; Pred. No. 5.2e-35;  
Matches 82; Conservative 15; Mismatches 21; Indels 8; Gaps 2;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
Db 3 QVQLHQSGPEVKKPGASVKLSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 62  
Qy 61 AQKFGQRTVMTDRTSISTAYMELSLRSEDTAIYVCVRFSGYSYNDYYGMDVWGQGT 119  
Db 63 NEKPKGRATLSVDKSSSTAYMELTRTSDSAVYICARG-----DYRRYFDLWGQGT 115  
  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 1.  
FT NON_TER 145  
SQ SEQUENCE 145 AA; 16081 MW; ECDLIAI35E05B8AA CRC64;  
  
Query Match 63.3%; Score 425.5; DB 11; Length 145;  
Best Local Similarity 64.8%; Pred. No. 2.2e-35;  
Matches 81; Conservative 17; Mismatches 22; Indels 5; Gaps 1;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
Db 1 QVQLQPGAEVKKPGASVKLSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
Qy 61 AQKFGQRTVMTDRTSISTAYMELSLRSEDTAIYVCVRFSGYSYNDYYGMDVWGQGT 120  
Db 61 NEKPKSKATLTVDPSSATAYMQLSLTSDSAVYICARS-----DYDYDYAMDYWGQGT 115  
  
Qy 121 TVTVSS 125  
Db 116 TVTVSS 120  
  
RESULT 15  
Q95978 PRELIMINARY; PRT; 157 AA.  
AC Q95978 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Vhl protein precursor (fragment).  
GN VHL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral blood;  
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,  
RA Bohlen H., Diehl V., Wolf J.;  
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a  
RT patient with mixed cellularly Hodgkin's disease is associated with  
RT somatic mutations within the untranslated regions of rearranged and  
RT class switch recombined Ig genes."  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ005570; CAA08599.1; --  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 1.  
KW Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT NON_TER 157  
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;  
  
Query Match 62.5%; Score 420; DB 4; Length 157;  
Best Local Similarity 67.5%; Pred. No. 9e-35;  
Matches 85; Conservative 13; Mismatches 22; Indels 6; Gaps 2;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
Db 20 QVQLVQSGAEIKPGASVKVCKTSYVFTSYIHWVRQPGQGLEWMGIGFGVGSTMC 79  
Qy 61 AQKFGQRTVMTDRTSISTAYMELSLRSEDTAIYVCVRFSGY-SYNDYYGMDVWGQGT 119  
Db 80 AEKFGRLTMTNTSTTTVTMELSLRFBTDATVYFCGRGRWSGNYNGH-----WGQGT 134  
  
Qy 120 TVTVSS 125  
Db 135 PVTVSS 140  
  
Search completed: April 21, 2004, 17:03:46  
Job time : 41.0901 secs
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OM protein - protein search, using sw model

Run on: April 21, 2004, 16:59:07 ; Search time 14.485 Seconds
(without alignments)
830.097 Million cell updates/sec

Title: US-10-041-860-48
Perfect score: 672
Sequence: 1 QVQLVQSGAEVKKPGASVK.....YDYVGMVWGQGTITVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	82.9	127	S34014	Ig heavy chain V r
2	537.5	80.0	136	S31600	Ig heavy chain V r
3	534	79.5	129	S46393	Ig heavy chain V r
4	516.5	76.9	118	S36265	Ig heavy chain V r
5	515	76.6	123	D33548	Ig heavy chain V-1
6	514	76.5	129	S36260	Ig heavy chain V r
7	511.5	76.1	135	S49530	anti-Sm antibody V
8	510.5	76.0	132	S31596	Ig heavy chain V r
9	500	74.4	131	S26792	Ig heavy chain V r
10	499	74.3	119	PH0961	Ig heavy chain V r
11	496.5	73.9	110	PH1670	Ig heavy chain V r
12	496	73.8	98	S26918	Ig heavy chain V r
13	495.5	73.7	132	PH0954	Ig heavy chain V r
14	495.5	73.7	171	S23623	Ig heavy chain V r
15	494.5	73.6	118	PH1666	Ig heavy chain V r
16	493.5	73.4	136	PH0960	Ig heavy chain V r
17	488.5	72.7	143	EHUND	Ig heavy chain pre
18	488	72.6	127	PH0955	Ig heavy chain V r
19	487.5	72.5	124	S19665	Ig heavy chain V r
20	486	72.3	133	S33548	Ig heavy chain V-1
21	486	72.3	627	S14683	Ig mu chain precu
22	484	72.0	142	A3483	Ig heavy chain V r
23	480	71.4	122	S36271	Ig heavy chain V r
24	480	71.4	160	FL0105	anti-PR2 erythrocy
25	477.5	71.1	126	S33548	Ig heavy chain V-1
26	476.5	70.9	114	PH1667	Ig heavy chain V r
27	473.5	70.5	128	PH0952	Ig heavy chain V r
28	472.5	70.3	120	S31999	Ig heavy chain V r
29	468	69.6	109	PH1668	Ig heavy chain V r

30 465 69.2 98 2 S26938 Ig heavy chain V r
31 465 69.2 117 2 S31680 Ig heavy chain V r
32 465 69.2 117 2 S18551 Ig heavy chain V r
33 465 69.2 126 2 S44151 Ig heavy chain V r
34 463 68.9 104 2 S69899 Ig heavy chain V r
35 462 68.8 121 2 S20783 Ig heavy chain V r
36 460.5 68.5 122 2 PH0958 Ig heavy chain V r
37 457 68.0 98 2 S26912 Ig heavy chain V r
38 456 67.9 125 2 PH0957 Ig heavy chain V r
39 455.5 67.8 120 2 S26789 Ig heavy chain V r
40 454.5 67.6 132 2 S46394 Ig heavy chain V-1
41 454 67.6 129 2 S33548 Ig heavy chain V r
42 452.5 67.3 110 2 PH1669 Ig heavy chain V r
43 449 66.8 125 2 S68170 Ig heavy chain V r
44 448.5 66.7 116 2 PH0959 Ig heavy chain V r
45 446.5 66.4 135 2 S32274 Ig heavy chain pre

ALIGNMENTS

RESULT 1
S34014
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S34014; S30535
R:Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Nucl. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34014
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-127 <NAR>
A:Cross-references: EMBL:Z18321
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 557; DB 2; Length 127;
Best Local Similarity 82.7%; Pred. No. 1.5e-42;
Matches 105; Conservative 10; Mismatches 10; Indels 2; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQVWSGAEVKKPGASVKSCASGYTFTSYDINNVRQATGQGLEWMGMMNPSSGNTGY 60
QY 61 AQKFGKRVMTWRTSTISITAYMELSLRSEDITAIYICVR--GFGYSYNYDYFYGMVWGOG 118
Db 61 AQKFGKRVMTWRTSTISITAYMELSLRSEDITAIYICVR--GFGYSYNYDYFYGMVWGOG 120
QY 119 TTVTVSS 125
Db 121 TTVSVSS 127

RESULT 2
S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 537.5; DB 2; Length 136;
Best Local Similarity 82.4%; Pred. No. 8.6e-41;
Matches 103; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTGY 79

QY 61 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 80 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120

QY 121 VTVSS 125
DB 131 VTVSS 135

RESULT 3

S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:Z31680; NID:G509786; PIDN:CAA83485.1; PID:gl335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 534; DB 2; Length 129;
Best Local Similarity 79.8%; Pred. No. 1.7e-40;
Matches 103; Conservative 7; Mismatches 15; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWNPNSGNTY 60

QY 61 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSYNDYYG---WDYWG 116
DB 61 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSYNDYYG---WDYWG 120

QY 117 QGTVTVSS 125
DB 121 KGTVTVSS 129

RESULT 4

S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18845; NID:G33121; PIDN:CAA79298.1; PID:G939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 516.5; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 5.4e-39;
Matches 100; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWNPNSGNTY 60

QY 61 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSYNDYYGMDVWGQGT 113

QY 121 VTVSS 125
DB 114 VTVSS 118

RESULT 5

D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp.
A;Reference number: A33548; MUID:189345575; PMID:2503826
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 515; DB 2; Length 123;
Best Local Similarity 78.6%; Pred. No. 7.6e-39;
Matches 99; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWNPNSGNTY 60

QY 61 AOKFQGRVTMTSDTSISTAYMELSLRSDTAIYVCVRGFGYSY-NDYYGMDVWGQGT 119
DB 61 AOKFQGRVTMTSDTSINTAYMELSLRSDTAIYVCARA---SYCGYDCYFFDYWGQGT 117

QY 120 TVTVSS 125
DB 118 LTVTVSS 123

RESULT 6

S36260
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36260
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-129 <GRI>
A;Cross-references: EMBL:Z18851; NID:G33124; PIDN:CAA79303.1; PID:G939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 514; DB 2; Length 129;
 Best Local Similarity 78.3%; Pred. No. 9.8e-39;
 Matches 101; Conservative 8; Mismatches 16; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 60
 QY 61 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSYNYD---YYTGMVDMVG 116
 DB 61 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSYNYD---YYTGMVDMVG 116
 QY 117 QGTTVTVSS 125
 DB 121 KGTTVTVSS 129

RESULT 7
 S49530
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
 C:Species: Homo sapiens (man)
 C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C:Accession: S49530
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S49530
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <MA>
 A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID:G560840
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 511.5; DB 2; Length 135;
 Best Local Similarity 79.4%; Pred. No. 1.7e-38;
 Matches 100; Conservative 6; Mismatches 9; Indels 11; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 60
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 79
 QY 61 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSYNYDYYTGMVDMVGQGT 119
 DB 80 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSYNYDYYTGMVDMVGQGT 129
 QY 120 TVTVSS 125
 DB 130 LVTVSS 135

RESULT 8
 S31596
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31596
 R:Cuissinier, A.M.; Gauchier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31596
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-132 <CU>
 A:Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 510.5; DB 2; Length 132;
 Best Local Similarity 79.2%; Pred. No. 2.1e-38;

Matches 99; Conservative 6; Mismatches 7; Indels 13; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 60
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 79
 QY 61 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSYNYDYYTGMVDMVGQGT 120
 DB 80 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSYNYDYYTGMVDMVGQGT 126
 QY 121 TVTVSS 125
 DB 127 TVTVSS 131

RESULT 9
 S26792
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26792
 R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
 Eur. J. Immunol. 22, 241-245, 1992
 A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam
 A:Reference number: S26786; MUID:92111632; PMID:1730251
 A:Accession: S26792
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-131 <MOR>
 A:Cross-references: EMBL:X61012; NID:G32804; PIDN:CAA43346.1; PID:G1335131
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 500; DB 2; Length 131;
 Best Local Similarity 72.5%; Pred. No. 1.7e-37;
 Matches 95; Conservative 13; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGMGWINPNSGNTDY 60
 QY 61 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSY---NYDYTGMVDMV 114
 DB 61 AQKFGQRTVMTDRDTSISTAYMELSLRSRSDTAIYYCVRG-FGYSY---NYDYTGMVDMV 120
 QY 115 WGQGTTVTVSS 125
 DB 121 WGKGTTVTVSS 131

RESULT 10
 PH0961
 Ig heavy chain V region (G6+ T-L33) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C:Accession: PH0961
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880; PMID:1552291
 A:Accession: PH0961
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-119 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3

F;99-107/Region: complementarity-determining 3

Query Match 74.3%; Score 499; DB 2; Length 119;
Best Local Similarity 79.2%; Pred. No. 1.9e-37;
Matches 99; Conservative 6; Mismatches 14; Indels 6; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCVRGYSYNYDYVYGMVWGQGT 120
DB 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCVRGYSYNYDYVYGMVWGQGT 114
QY 121 VTSS 125
DB 115 VTSS 119

RESULT 11

PH1670
IG heavy chain V region (clone 2A12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1670
R: Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315386
A:Accession: PH1670
A:Molecule type: mRNA
A:Residues: 1-110 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 496.5; DB 2; Length 110;
Best Local Similarity 82.1%; Pred. No. 3e-37;
Matches 96; Conservative 6; Mismatches 8; Indels 7; Gaps 2;
QY 9 AEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAKKFGQVR 68
DB 1 AEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAKKFGQVR 60
QY 69 TMTDTSISTAYMELSLRSEDATAYVCVRGYSYNYDYVYGMVWGQGT 125
DB 61 TMTDTSISTAYMELSLRSEDATAYVCVRGYSYNYDYVYGMVWGQGT 110

RESULT 12

S26918
IG heavy chain V region (DP-15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918
R: Tomlinson, I.N.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) segments
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26918
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12317; NID:G32857; PIDN:CAA78187.1; PID:G32858
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 496; DB 2; Length 98;
Best Local Similarity 94.9%; Pred. No. 2.9e-37;
Matches 93; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCVR 98
DB 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCAR 98

RESULT 13

PH0954
IG heavy chain V region (G6+ CLL-HEN) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0954
R: Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0954
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-132 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

Query Match 73.7%; Score 495.5; DB 2; Length 132;
Best Local Similarity 75.9%; Pred. No. 4.4e-37;
Matches 101; Conservative 6; Mismatches 17; Indels 9; Gaps 2;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPQGLEWMGWIPIFGTANY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCVRGFI 112
DB 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCARPHASIDDFWSGYNY-YVYGM 119

Query Match 73.7%; Score 495.5; DB 2; Length 132;
Best Local Similarity 75.9%; Pred. No. 4.4e-37;
Matches 101; Conservative 6; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPQGLEWMGWIPIFGTANY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCVRGFI 112
DB 61 AQKFGQRTVTRDTSISTAYMELSLRSEDATAYVCARPHASIDDFWSGYNY-YVYGM 119

RESULT 14

S23623
IG heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R: Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from patients with rheumatoid arthritis
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23623
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:Cross-references: EMBL:X59702; NID:G32010; PIDN:CAA42223.1; PID:G32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 495.5; DB 2; Length 171;
Best Local Similarity 70.9%; Pred. No. 5.8e-37;
Matches 95; Conservative 9; Mismatches 13; Indels 17; Gaps 2;

```
Qy 1 QVQLVQSGAEVKPGASVKSCAKSCTYSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 20 QVQLVQSGAEVKPGASVKSCAKSCTYSYDINWVRQATGQGLEWMGWINPNSGNTDY 79
Qy 61 AQKFQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYYG----- 111
Db 80 GQKFQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYYG----- 131
Qy 112 MDVWGQGTITVTVSS 125
Db 132 FDIWGQGTMTVTVSS 145

RESULT 15
PH1666
Ig heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1666
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1666
A;Molecule type: mRNA
A;Residues: 1-118 <Hil>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 494.5; DB 2; Length 118;
Best Local Similarity 80.5%; Pred. No. 4.8e-37;
Matches 95; Conservative 6; Mismatches 16; Indels 1; Gaps 1;

Qy 9 AEVKKPGASVKSCAKSCTYSYDINWVRQATGQGLEWMGWINPNSGNTDYAKKFGGRV 68
Db 1 AEVKKPGASVKSCAKSCTYSYDINWVRQATGQGLEWMGWINAGNTKYAKKFGGRV 60
Qy 69 TMTDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGTITVTVSS 125
Db 61 TITDTSASTAYMELSLRSEDTAIYYCARVTLDDGKIFYYGMDVWGQGTITVTVSS 118
```

Search completed: April 21, 2004, 17:04:24
Job time : 15.485 secs


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Db 20 QTQLVQSGAEVRKPGASVVRVSKASGYTFIDSYIHWRQAPGHLEWVGWINPNSGGTNY 79
Qy 61 AQKFGQVMTTRDTSISTAYMELSLRSDTAIYVCVRG---FGYSVNYDYVYGMVDVWQ 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 APFQFQVMTTRDTSISTAYMELSLRSDTAIYVCVRG---FGYSVNYDYVYGMVDVWQ 139
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 118 GTTIVTSS 125
      :|||||:
Db 140 GTTIVTSS 147
      :|||||:

RESULT 2
HV1G HUMAN STANDARD; PRT; 117 AA.
AC P23083;
AT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07448; -; NOT ANNOTATED_CDS.
DR PIR; S00476; HVHJ35.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0004955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 65.6%; Score 441; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3e-37;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVCASGYSYTFSTVDINWVRQATGQGLEWMGWINPNSGNTDY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKPGASVKVCASGYSYTFSTVDINWVRQAPGQGLEWMGWINPNSGGTNY 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AQKFGQVMTTRDTSISTAYMELSLRSDTAIYVCVR 98
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AQKFGQVMTTRDTSISTAYMELSLRSDTAIYVCVR 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
HV1G HUMAN STANDARD; PRT; 117 AA.
AC P23083;
AT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07448; -; NOT ANNOTATED_CDS.
DR PIR; S00476; HVHJ35.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0004955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 65.6%; Score 441; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3e-37;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVCASGYSYTFSTVDINWVRQATGQGLEWMGWINPNSGNTDY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKPGASVKVCASGYSYTFSTVDINWVRQAPGQGLEWMGWINPNSGGTNY 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AQKFGQVMTTRDTSISTAYMELSLRSDTAIYVCVR 98
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AQKFGQVMTTRDTSISTAYMELSLRSDTAIYVCVR 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
HV51 MOUSE STANDARD; PRT; 118 AA.
ID HV51 MOUSE
AC P06330;
AT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

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RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MEMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEB4C762A018 CRC64;

Query Match 62.3%; Score 418.5; DB 1; Length 118;
Best Local Similarity 63.2%; Pred. No. 5.4e-35;
Matches 79; Conservative 15; Mismatches 24; Indels 7; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYIMWVWKQSHGKSLWIGDINPNSGTSY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSSLRSEDTAIYVCVRFSGYSYNYDYVGMVWGQTT 120
DB 61 NQKFKGKATLTVDKSSATYMLRSLTSEDSAVYYCARGYGYD-----PFVWGTT 113
QY 121 VTSS 125
DB 114 VTSS 118

RESULT 5
HV12 MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02039; MEMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117

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SQ SEQUENCE 117 AA; 12983 MW; 3CFBACE4BE447B41 CRC64;

Query Match 61.6%; Score 414; DB 1; Length 117;
Best Local Similarity 63.2%; Pred. No. 1.5e-34;
Matches 79; Conservative 19; Mismatches 19; Indels 8; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYIMWVWKQSHGKSLWIGDINPNSGTSY 60
QY 61 AQKFGQRTVTRDTSISTAYMELSSLRSEDTAIYVCVRFSGYSYNYDYVGMVWGQTT 120
DB 61 NQKFKGKATLTVDKSSATYMLRSLTSEDSAVYYCAR-----DYDWYF--DWGAGTT 112
QY 121 VTSS 125
DB 113 VTSS 117

RESULT 6
HV03 MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131646; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 61.5%; Score 413; DB 1; Length 120;
Best Local Similarity 62.7%; Pred. No. 1.9e-34;
Matches 79; Conservative 19; Mismatches 20; Indels 8; Gaps 2;

QY 2 VOLVQSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYA 61
DB 1 VOLQQSGAEVLVRAGSSVKMSCKASGYTFTSYGINWVKQPGQGLEWIGYINPGNYTKYN 60
QY 62 QKFGQRTVTRDTSISTAYMELSSLRSEDTAIYVCVTFG--FGSYNYDYVGMVWGQTT 119
DB 61 EKFKGKATLTVDKSSATYMLRSLTSEDSAVYYGGSYYFYD-----WGQGT 114
QY 120 VTSS 125
DB 115 TLTVSS 120

RESULT 7

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HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234549; PubMed=6783376;
RA Bathwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL; J00529; AAA38170.1; -
DR PIR; A90809; MHMS18.
DR PDB; 1A6U; 27-MAY-98.
DR PDB; 1A6W; 15-JUL-98.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 60.8%; Score 408.5; DB 1; Length 139;
Best Local Similarity 63.0%; Pred. No. 6.4e-34;
Matches 80; Conservative 16; Mismatches 22; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRCATGQGLEWMGWINPNSGNTDY 60
DB 20 QVQLQPGAEVKKPGASVKLSCKASGYTFTSYDINWVRCATGQGLEWMGWINPNSGNTDY 79
QY 61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYCYVRGFGYSYNDYYG--MDVWQGG 118
DB 80 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYYCAR-----YDYVGSFYDWQGG 132
QY 119 TTVVSS 125
DB 133 TITLVSS 139

RESULT 8

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HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 60.7%; Score 408; DB 1; Length 117;
Best Local Similarity 62.4%; Pred. No. 5.9e-34;
Matches 78; Conservative 17; Mismatches 22; Indels 8; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRCATGQGLEWMGWINPNSGNTDY 60
DB 1 EVQLQSGPELVKPGASVKVSCKASGYTFTSYDINWVRCATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYCYVRGFGYSYNDYYGMDVWQGGTT 120
DB 61 NQKFKSKATLTVDKSSSTAYMQLSLTSDSAVYYCAR-----DRYWFYDWAGGTT 112
QY 121 TTVSS 125
DB 113 TTVSS 117

RESULT 9
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Bates P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";

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RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J00493; AAA38128.1; --
DR PIR: A94264; HVMSG7.
DR HSSP: P01810; 2FSJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS08335; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBEB31DA5CE8 CRC64;

Query Match 60.7%; Score 408; DB 1; Length 140;
Best Local Similarity 60.8%; Pred. No. 7.3e-34;
Matches 76; Conservative 21; Mismatches 24; Indels 4; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60
DB 20 EVQLQSGAEVLRAGSSVKKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 79

QY 61 AOKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGOGTT 120
DB 80 NEKFKKATLTVDKSSATYMQLRSLTSDSAVYFCARSHYVGGSYDP----DWVGQGT 135

QY 121 VTVSS 125
DB 136 LTVSS 140

RESULT 10
HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EWO J. 3:517-523(1984).
DR PIR: A02037; MEMS15.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS08335; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT NON_TER 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.

FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453P426F09834 CRC64;

Query Match 58.7%; Score 394.5; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 1.4e-32;
Matches 75; Conservative 20; Mismatches 25; Indels 5; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60
DB 1 QVQLLPQGTETLVKPGASVNLKSKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60

QY 61 AOKFGQGRVTMTDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGOGTT 120
DB 61 NEKFKKATLTVDKSSATYMQLRSLTSDSAVYFCAR---WDYEGDRYF--DWVGNGTT 115

QY 121 VTVSS 125
DB 116 VTVSS 120

RESULT 11
HV1A HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Wexler M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90563; G1HUEU.
DR HSSP: P01772; 2FBA.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0008955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS08335; IG LIKE; 1.
KW Immunoglobulin V region; Pyridoxine carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 58.0%; Score 390; DB 1; Length 117;
Best Local Similarity 67.2%; Pred. No. 3.7e-32;
Matches 84; Conservative 9; Mismatches 24; Indels 8; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTDY 60


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Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGFTFSRLTIIVRQAPGQGLRWGIVPMFGPPNY 60
Qy 61 AQKFGQGRVTMTDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120
Db 61 AQKFGQGRVTMTDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120
Qy 121 VTVSS 125
Db 113 VTVSS 117

RESULT 12
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paikind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_v.
DR SMART; SM00406; IGV.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 63 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF4B8EC9 CRC64;

Query Match 57.8%; Score 388.5; DB 1; Length 137;
Best Local Similarity 61.6%; Pred. No. 6.2e-32;
Matches 77; Conservative 15; Mismatches 26; Indels 7; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGFTFSRLTIIVRQAPGQGLRWGIVPMFGPPNY 60
Db 20 QVQLQPGAEVKKPGASVKLSCKASGFTFSRLTIIVRQAPGQGLRWGIVPMFGPPNY 79

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Qy 61 AQKFGQGRVTMTDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120
Db 80 NEHFRSKATLIDKPSSTAYMQLSSLTSEDSAVTYCAR-----YRLGRYF--DYWGQGT 132
Qy 121 VTVSS 125
Db 133 VTVSS 137

RESULT 13
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region TPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMS77.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG.
DR SMART; SM00406; IGV.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 FRAMEWORK-4.
FT DOMAIN 128 138 BY SIMILARITY.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 57.0%; Score 383; DB 1; Length 138;
Best Local Similarity 59.2%; Pred. No. 2.2e-31;
Matches 74; Conservative 20; Mismatches 25; Indels 6; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGFTFSRLTIIVRQAPGQGLRWGIVPMFGPPNY 60
Db 20 QVQLQPGAEVKKPGASVKLSCKASGFTFSRLTIIVRQAPGQGLRWGIVPMFGPPNY 79
Qy 61 AQKFGQGRVTMTDTSISTAYMELSSLSRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120
Db 80 NEKFKKATLTVDKSSSTAYMQLSSLTPEEFAVYICARSDGY---YDFV---YWGQGT 133
Qy 121 VTVSS 125
Db 134 VTVSS 138

RESULT 14
HV1F HUMAN
ID HV1F HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)

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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG heavy chain V-I region Mot.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=86203277; PubMed=3084950;
Kojima M., Koide T., Odani S., Ono T.;
"Amino acid sequence of the variable region of heavy chain in
immunoglobulin (Mot) having unusual papain cleavage sites.";
Mol. Immunol. 23:169-174(1986).
PIR; A02025; HVHUM0.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 107 D SEGMENT.
FT DOMAIN 108 125 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 56.2%; Score 378; DB 1; Length 125;
Best Local Similarity 58.4%; Pred. No. 6.3e-31;
Matches 73; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGSSARLSCKVSGDDFNTYDIHWVRQAPGRGLEWMAVVPSPDRTTY 60

QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVSGFGYSYNYDYVYGMVWGQGT 120
Db 61 GPRSQARFTVTRDSSTTVYMETALISADTAIYVCARGAHYSDDTDDSGTSLGPGWQGT 120

QY 121 VTVSS 125
Db 121 LIVSS 125

RESULT 15
HV01 MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED

FROM A MYELOMA THAT SECRETES IGG2B.
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVM511.
DR HSSP; P01810; 2FB7.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 56.0%; Score 376; DB 1; Length 121;
Best Local Similarity 58.4%; Pred. No. 9.6e-31;
Matches 73; Conservative 19; Mismatches 29; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 EAQLQSGAEVLRPGTSVKISKAAGYFTNTWIGVKERPGHLEWIGDIYFGGFTNY 60

QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVSGFGYSYNYDYVYGMVWGQGT 120
Db 61 NDNLKGTATLTADTSSTAYIQLSLTSDSAIYHCARGI---YINSSPIF---DSWGQGT 116

QY 121 VTVSS 125
Db 117 LIVSS 121

Search completed: April 21, 2004, 17:02:34
Job time : 26.2661 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 19.2464 Seconds

(without alignments)

42.918 Million cell updates/sec

Title: SEQ3

Perfect score: 97

Sequence: 1 gfgysynydyvgmdv 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	52	53.6	24	US-09-142-732-4	Sequence 4, Appli
2	52	53.6	522	US-09-142-732-2	Sequence 2, Appli
3	52	53.6	522	US-08-945-826-2	Sequence 2, Appli
4	52	53.6	522	US-09-197-503-2	Sequence 2, Appli
5	52	53.6	733	US-09-328-352-5599	Sequence 5599, Ap
6	50.5	52.1	36	US-08-053-131-84	Sequence 84, Appl
7	50.5	52.1	36	US-08-645-641-84	Sequence 84, Appl
8	50.5	52.1	36	US-07-853-408B-84	Sequence 84, Appl
9	50.5	52.1	36	US-08-096-762-84	Sequence 84, Appl
10	50.5	52.1	36	US-08-308-865-84	Sequence 84, Appl
11	50.5	52.1	36	US-09-042-353-281	Sequence 129, App
12	50.5	52.1	36	US-08-758-417A-129	Sequence 129, App
13	50.5	52.1	36	PCT-US92-10983-84	Sequence 84, Appl
14	48	49.5	126	US-08-983-607-48	Sequence 48, Appl
15	48	49.5	287	US-08-862-124-17	Sequence 17, Appl
16	48	49.5	304	US-08-862-124-14	Sequence 14, Appl
17	48	49.5	521	US-08-945-826-4	Sequence 4, Appli
18	48	49.5	521	US-09-197-503-4	Sequence 4, Appli
19	47.5	49.0	123	US-08-652-816A-1	Sequence 1, Appli
20	47.5	49.0	123	US-08-652-816A-6	Sequence 6, Appli
21	47.5	49.0	236	US-09-456-090A-64	Sequence 64, Appl
22	47.5	49.0	236	US-09-456-090A-104	Sequence 104, App
23	46	47.4	29	US-08-053-131-73	Sequence 73, Appl
24	46	47.4	29	US-08-643-641-73	Sequence 73, Appl
25	46	47.4	29	US-07-853-408B-73	Sequence 73, Appl
26	46	47.4	29	US-08-096-762-73	Sequence 73, Appl
27	46	47.4	29	US-08-308-865-73	Sequence 73, Appl

Sequence 270, App
Sequence 118, App
Sequence 73, Appl
Sequence 80, Appl
Sequence 70, Appl
Sequence 282, App
Sequence 25, Appl
Sequence 26, Appl
Sequence 153, App
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 3, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 34, Appl
Sequence 6014, Ap
Sequence 5, Appli

28 46 47.4 29 3 US-09-042-353-270
29 46 47.4 29 4 US-08-758-417A-118
30 46 47.4 29 5 PCT-US92-10983-73
31 46 47.4 167 4 US-09-472-087-80
32 46 47.4 451 4 US-09-472-087-70
33 46 47.4 633 4 US-09-976-594-282
34 45.5 46.9 126 3 US-09-240-274-25
35 45.5 46.9 126 3 US-09-240-274-153
36 45.5 46.9 126 3 US-09-240-274-153
37 45 46.4 23 1 US-08-004-139B-35
38 45 46.4 23 2 US-08-811-492-35
39 45 46.4 23 5 PCT-US96-10545A-35
40 45 46.4 123 1 US-08-082-623-3
41 45 46.4 128 1 US-08-478-039-96
42 45 46.4 128 1 US-08-478-349A-96
43 45 46.4 391 4 US-09-721-870-34
44 45 46.4 408 4 US-09-328-352-6014
45 44.5 45.9 1326 4 US-09-147-236-5

ALIGNMENTS

RESULT 1

US-09-142-732-4
; Sequence 4, Application US/09142732
; Patent No. 6252045
; GENERAL INFORMATION:
; APPLICANT: James M. Anderson
; APPLICANT: Christina M. Van Itallie
; TITLE OF INVENTION: Human Occludin, Its Uses and
; TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin Inhibitors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yale University Medical School
; ADDRESSEE: Section of Digestive Diseases
; ADDRESSEE: Department of Internal Medicine
; STREET: 333 Cedar Street, LCI 105
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8057
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,732
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/05909
; FILING DATE: March 14, 1997
; APPLICATION NUMBER: U.S. 60/013,625
; FILING DATE: March 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-324-6155
; TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: synthetic peptide
; FEATURE:

OTHER INFORMATION: construct used in experi-
OTHER INFORMATION: ments

US-09-142-732-4

Query Match 53.6%; Score 52; DB 3; Length 24;
Best Local Similarity 61.5%; Pred. No. 0.3;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
|:|:|:|:|:|:|
Db 6 GVGYGYGYG 18

RESULT 2

US-09-142-732-2
Sequence 2, Application US/09142732
Patent No. 6252045
GENERAL INFORMATION:
APPLICANT: James M. Anderson
APPLICANT: Christina M. Van Itallie
TITLE OF INVENTION: Human Occludin, Its Uses and
TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin Inhibitors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University Medical School
ADDRESSEE: Section of Digestive Diseases
ADDRESSEE: Department of Internal Medicine
STREET: 333 Cedar Street, LCI 105
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8057
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,732
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/05809
FILING DATE: March 14, 1997
APPLICATION NUMBER: U.S. 60/013,625
FILING DATE: March 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 522
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
FRAGMENT TYPE: complete sequence
FEATURE:
NAME/KEY: human occludin
US-09-142-732-2

Query Match 53.6%; Score 52; DB 3; Length 22;
Best Local Similarity 61.5%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
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Db 117 GVGYGYGYG 129

RESULT 3

US-08-945-826-2
Sequence 2, Application US/08945826
Patent No. 6489460
GENERAL INFORMATION:
APPLICANT: TSUKITA, Shoichiro
TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,826
FILING DATE: 05-NOV-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARACI, C. Joseph
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 0425-0660P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-945-826-2

Query Match 53.6%; Score 52; DB 4; Length 522;
Best Local Similarity 61.5%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
|:|:|:|:|:|:|
Db 117 GVGYGYGYG 129

RESULT 4

US-09-197-503-2
Sequence 2, Application US/09197503
Patent No. 6559286
GENERAL INFORMATION:
APPLICANT: TSUKITA, Shoichiro
TITLE OF INVENTION: HUMAN ADHESION MOLECULE OCCLUDIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,503
FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/945,826
; FILING DATE: 05-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. Joseph
; REGISTRATION NUMBER: 32,350
; REFERENCE/DOCKET NUMBER: 0425-0660P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 522 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-197-503-2

Query Match 53.6%; Score 52; DB 4; Length 522;
Best Local Similarity 61.5%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
Db 117 GYGYGYGYG 129

RESULT 5
US-09-328-352-5599
; Sequence 5599, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5599
; LENGTH: 733
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-5599

Query Match 53.6%; Score 52; DB 4; Length 733;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 12
Db 716 GYGYGYNAYAY 727

RESULT 6
US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-053-131-84

Query Match 52.1%; Score 50.5; DB 1; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
Db 11 SYDY-YYGMDV 21

RESULT 7
US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; COMPUTER READABLE FORM:

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;
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-645-641-84

Query Match 52.1%; Score 50.5; DB 1; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDDYYGMDV 16
Db 11 SYDY-YYGMDV 21

RESULT 8
US-07-853-408B-84
; Sequence 84, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-853-408B-84

Query Match 52.1%; Score 50.5; DB 1; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDDYYGMDV 16
Db 11 SYDY-YYGMDV 21

RESULT 9
US-08-096-762-84
; Sequence 84, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-096-762-84

Query Match 52.1%; Score 50.5; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDDYYGMDV 16
Db 11 SYDY-YYGMDV 21

RESULT 10
US-08-308-865-84
; Sequence 84, Application US/08308865
; Patent No. 5877397
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
```

APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE: 23-JUN-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE: 23-JUN-1992
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-84

Query Match 52.1%; Score 50.5; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
DB 11 SYDY-YYGMDV 21

RESULT 11
US-09-042-353-281
Sequence 281, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE: 23-JUN-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE: 23-JUN-1992
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-84

Query Match 52.1%; Score 50.5; DB 3; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
DB 11 SYDY-YYGMDV 21

RESULT 11
US-09-042-353-281
Sequence 281, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-281

Query Match 52.1%; Score 50.5; DB 3; Length 36;
Best Local Similarity 83.3%; Pred. No. 0.75;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 5 SYNDYYGMDV 16
DB 11 SYDY-YYGMDV 21

RESULT 11
US-09-042-353-281
Sequence 281, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Db 11 SYDY-YYGMDV 21

RESULT 12

US-08-758-417A-129

; Sequence 129, Application US/08758417A

; Patent No. 63001129

; GENERAL INFORMATION:

; APPLICANT: Lomberg, Nils

; Kay, Robert M.

; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for

; Producing Heterologous Antibodies

; NUMBER OF SEQUENCES: 417

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/758,417A

; FILING DATE: 02-Dec-1996

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/728,463

; FILING DATE: 10-OCT-1996

; APPLICATION NUMBER: US 08/544,404

; FILING DATE: 10-OCT-1995

; APPLICATION NUMBER: US 08/352,322

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: US 08/209,741

; FILING DATE: 09-MAR-1994

; APPLICATION NUMBER: US 08/165,699

; FILING DATE: 10-DEC-1993

; APPLICATION NUMBER: US 08/161,739

; FILING DATE: 03-DEC-1993

; APPLICATION NUMBER: US 08/155,301

; FILING DATE: 18-NOV-1993

; APPLICATION NUMBER: US 08/096,762

; FILING DATE: 22-JUL-1993

; APPLICATION NUMBER: US 08/053,131

; FILING DATE: 26-APR-1993

; APPLICATION NUMBER: US 07/990,860

; FILING DATE: 16-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Serafini, Andrew T.

; REGISTRATION NUMBER: 41,303

; REFERENCE/DOCKET NUMBER: 014643-009030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 129:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 129:

US-08-758-417A-129

Query Match 52.1%; Score 50.5; DB 4; Length 36;

Best Local Similarity 83.3%; Pred. No. 0.75;

Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Oy 5 SYNDYYGMDV 16

Db 11 SYDY-YYGMDV 21

RESULT 13

PCT-US92-10983-84

; Sequence 84, Application PC/TUS9210983

; GENERAL INFORMATION:

; APPLICANT: Lomberg, Nils

; Kay, Robert M.

; TITLE OF INVENTION: Transgenic Non-Human Animals for

; Producing Heterologous Antibodies

; NUMBER OF SEQUENCES: 152

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: William M. Smith

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/10983

; FILING DATE: 19921217

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 14643-9-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; PCT-US92-10983-84

Query Match 52.1%; Score 50.5; DB 5; Length 36;

Best Local Similarity 83.3%; Pred. No. 0.75;

Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Oy 5 SYNDYYGMDV 16

Db 11 SYDY-YYGMDV 21

RESULT 14

US-08-983-607-48

; Sequence 48, Application US/08983607

; Patent No. 6140470

; GENERAL INFORMATION:

; APPLICANT: Alan Garen

; APPLICANT: Xiaohong Cai

; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-

; bodies

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Department of Molecular Biophysics

; and Biochemistry, Yale University

; STREET: 266 Whitney Avenue

; CITY: New Haven

; STATE: Connecticut

; COUNTRY: United States of America

; ZIP: 06520-8114

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" 1.44 Mb diskette


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; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983.607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient)
; ORGANISM: immunized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lympho-
; INDIVIDUAL ISOLATE: cytes
; IMMEDIATE SOURCE:
; LIBRARY: VH antibodies obtained from FUSE5
; LIBRARY: fusion phage construct
; CLONE: F2
; FEATURE:
; NAME/KEY: heavy chain
;
US-08-983-607-48

Query Match 49.5%; Score 48; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DYIYGVNDV 16
Db 108 DYIYGVNDV 115

RESULT 15
US-08-862-124-17
; Sequence 17, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862.124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-862-124-17

Query Match 49.5%; Score 48; DB 3; Length 287;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NYDYIYGVNDV 16
Db 247 DYDHYIYGLDV 256

Search completed: April 21, 2004, 17:40:04
Job time : 20.2464 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 14.6087 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ3
Perfect score: 97
Sequence: 1 gfgysynydyvgmdv 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	62.9	116	2 S37456	Ig mu chain - huma
2	58	59.8	205	2 F87623	hypothetical prote
3	55.5	57.2	19	2 PH1304	Ig heavy chain DJ
4	55	56.7	825	2 S64783	probable membrane
5	54.5	56.2	19	2 PH1307	Ig heavy chain DJ
6	53	54.6	45	2 PH0094	Ig heavy chain V r
7	52.5	54.1	132	2 PH0954	Ig heavy chain V r
8	52	53.6	522	2 G02533	Occludin - human
9	51	52.6	726	2 T44825	hypothetical prote
10	50.5	52.1	125	2 S24686	Ig heavy chain V6
11	50	51.5	110	2 PH1655	Ig heavy chain V r
12	49.5	51.0	29	2 PH1328	Ig heavy chain DJ
13	49	50.5	153	2 S31689	Ig heavy chain V r
14	49	50.5	1044	2 H37186	glycosyltransferas
15	48.5	50.0	128	2 S48797	Ig heavy chain V r
16	48.5	50.0	131	2 S26792	Ig heavy chain V r
17	48	49.5	24	2 P70258	Ig heavy chain CDR
18	48	49.5	97	2 S24252	Ig heavy chain V r
19	48	49.5	121	2 S31106	Ig heavy chain - h
20	48	49.5	146	1 PH1H02	Ig heavy chain pre
21	47.5	49.0	23	2 PH1361	Ig heavy chain DJ
22	47.5	49.0	105	2 H81723	hypothetical prote
23	47	48.5	23	2 PH1364	Ig heavy chain DJ
24	47	48.5	70	2 C83831	hypothetical prote
25	47	48.5	345	2 S23862	hypothetical prote
26	47	48.5	504	2 A49467	occludin - chicken
27	47	48.5	719	2 S63392	probable membrane
28	47	48.5	1048	2 H64459	hypothetical prote
29	46.5	47.9	45	2 S20776	Ig heavy chain V r

30	46	47.4	119	2 E25114	Ig heavy chain V r
31	46	47.4	119	2 PH0961	Ig heavy chain V r
32	46	47.4	127	2 PH0955	Ig heavy chain V r
33	46	47.4	132	2 AB1125	hypothetical prote
34	46	47.4	201	2 S37847	hypothetical prote
35	46	47.4	210	2 C87305	hypothetical prote
36	46	47.4	483	2 E90159	hypothetical prote
37	46	47.4	633	2 T02673	heterogeneous nucl
38	45.5	46.9	27	2 PH1355	Ig heavy chain DJ
39	45.5	46.9	27	2 PH1371	Ig heavy chain DJ
40	45.5	46.9	113	2 S30515	wound-induced prot
41	45.5	46.9	136	2 PH0980	Ig heavy chain V r
42	45	46.4	69	2 A64961	outer membrane por
43	45	46.4	120	2 PH1650	Ig heavy chain V r
44	45	46.4	122	2 T05357	ubiquinol-cytochro
45	45	46.4	136	2 A49047	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S37456
Ig mu chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R:Accession: S37456
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
Submitted to the EMBL Data Library, September 1993
A:Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from I
A:Reference number: S37453
A:Accession: S37456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <MC>
A:Cross-references: EMBL:X75024; NID:G404313; PIDN:CAA52932.1; PID:G758095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:6-90/Domain: immunoglobulin homology <IMV>

Query Match 62.9%; Score 61; DB 2; Length 116;
Best Local Similarity 78.6%; Pred. No. 0.098; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 3 GYSYNYDYVYGMVDV 16
DB 92 GYSYGYVYVYVMDV 105

RESULT 2

F87623
hypothetical protein CC3024 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: F87623
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.N.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87623
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <STO>
A:Cross-references: GB:AE005673; NID:G1342464; PIDN:AAK24986.1; GSPDB:GN00148
C:Genetics: CC3024

Query Match 59.8%; Score 58; DB 2; Length 205;
Best Local Similarity 58.8%; Pred. No. 0.46;
Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 GFGSYNYDY-----YTG 13
 Db 165 GYGVDYDYAPRPYTG 181

RESULT 3

PH1304
 Ig heavy chain DJ region (clone C439-111) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 R/Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1304
 A/Molecule type: DNA
 A/Residues: 1-19 <WAS>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 57.2%; Score 55.5; DB 2; Length 19;
 Best Local Similarity 78.6%; Pred. No. 0.087;
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 GYSYNYDYGYGMDV 16
 Db 2 GYFYNY-YTYGMDV 14

RESULT 4

S64783
 probable membrane protein YL032C - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein L0926
 C/Species: Saccharomyces cerevisiae
 C/Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
 R/Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64775
 A/Accession: S64783
 A/Molecule type: DNA
 A/Residues: 1-825 <DUE>
 A/Cross-references: EMBL:Z73137; NID:G1360217; PID:e245752; PID:G1360218; GSPDB:GN00012;
 A/Experimental source: strain S288C
 C/Genetics:
 A/Gene: MIPS:YL032C
 A/Cross-references: SGD:S0003955
 A/Map position: 12L
 C/Keywords: transmembrane protein
 F:660-676/Domain: transmembrane #status predicted <TMM>

Query Match 56.7%; Score 55; DB 2; Length 825;
 Best Local Similarity 66.7%; Pred. No. 5.2;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGSYNYDY 12
 Db 795 GYGTYEYDNY 806

RESULT 5

PH1307
 Ig heavy chain DJ region (clone C96-119) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 R/Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1307
 A/Molecule type: DNA

A/Residues: 1-19 <WAS>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 56.2%; Score 54.5; DB 2; Length 19;
 Best Local Similarity 78.6%; Pred. No. 0.12;
 Matches 11; Conservative 0; Mismatches 3; Indels 1;

QY 3 GYSYNYDYGYGMDV 16
 Db 4 GYSY---YTYGMDV 14

RESULT 6

PH0094
 Ig heavy chain V region (6C4) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 30-May-1997
 C/Accession: P00094
 R/Meek, K.; Hagemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Cai
 J. Exp. Med. 169, 519-533, 1989
 A/Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are
 A/Reference number: P00080; MUID:89094248; PMID:2492056
 A/Accession: P00094
 A/Molecule type: mRNA
 A/Residues: 1-45 <MEB>
 A/Note: the authors translated the codons AGC and AGU for residues 6 and 7 as Asp
 A/Note: the sequence shown here is from the VH region of a syngeneic antibody to anti-3-1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 54.6%; Score 53; DB 2; Length 45;
 Best Local Similarity 81.8%; Pred. No. 0.47;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SYNYDYGYGMD 15
 Db 23 SYGYTYGYGMD 33

RESULT 7

PH0954
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0954
 R/Martin, I.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:9202880; PMID:1552291
 A/Accession: PH0954
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-132 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-120/Region: complementarity-determining 3

Query Match 54.1%; Score 52.5; DB 2; Length 132;
 Best Local Similarity 78.6%; Pred. No. 1.7;
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 GYSYNYDYGYGMDV 16
 Db 109 GYFNY-YTYGMDV 121

```

RESULT 8
G02533
occludin - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
C:Accession: G02533
R:Van Itallie, C.M.
submitted to the EMBL Data Library, April 1996
A:Reference number: H01403
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: G02533
A:Molecule type: mRNA
A:Residues: 1-522 <VAN>
A:Cross-references: EMBL:U53823; NID:g1322281; PIDN:AAB00195.1; PID:g1322282
C:Superfamily: occludin

Query Match      53.6%; Score 52; DB 2; Length 522;
Best Local Similarity 61.5%; Pred. No. 8.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 13
DB 117 GYGYGYGYG 129

RESULT 9
T44825
hypothetical protein wzc [imported] - Acinetobacter lwoffii
N:Alternate names: protein tyrosine kinase
C:Species: Acinetobacter lwoffii
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44825
R:Nakar, D.; Gutnick, D.L.
submitted to the EMBL Data Library, July 1999
A:Description: Genomic organization of the wzc region of Acinetobacter lwoffii RAG-1 re
A:Reference number: Z22856
A:Accession: T44825
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-726 <NA>
A:Cross-references: EMBL:AJ243431; PIDN:CAB57193.1
A:Experimental source: strain RAG-1
C:Genetics:
A:Gene: wzc

Query Match      52.6%; Score 51; DB 2; Length 726;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYG 12
DB 709 GAGYSYNAYAY 720

RESULT 10
S24686
Ig heavy chain V6 region - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S24686
R:van Es, J.H.
submitted to the EMBL Data Library, July 1992
A:Reference number: S24679
A:Accession: S24686
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <VAN>
A:Cross-references: EMBL:X67880; NID:g37749; PIDN:CAA48079.1; PID:g37750
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-101/Domain: immunoglobulin homology <IMM>

Query Match      52.1%; Score 50.5; DB 2; Length 125;

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```

Best Local Similarity 71.4%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 3 GYSYNDYYGMDV 16
DB 104 GYDY--YYGMDV 114

RESULT 11
PH1655
Ig heavy chain V region (clone 228) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1655
R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1655
A:Molecule type: mRNA
A:Residues: 1-110 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      51.5%; Score 50; DB 2; Length 110;
Best Local Similarity 69.2%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSYNDYYGMDV 16
DB 87 YCAREDDYYGMDV 99

RESULT 12
PH1328
Ig heavy chain DJ region (clone C113-148) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1328
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1328
A:Molecule type: DNA
A:Residues: 1-29 <WAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match      51.0%; Score 49.5; DB 2; Length 29;
Best Local Similarity 71.4%; Pred. No. 0.92;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 3 GYSYNDYYGMDV 16
DB 12 GSCYSY-YYGMDV 24

RESULT 13
S31689
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S31689
R:Cuisinier, A.M.; Gauthier, L.; Boulbi, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31689
A:Status: preliminary
A:Molecule type: mRNA

```

A;Residues: 1-153 <CUI>
A;Cross-references: EMBL:Z14187; NID:G31041; PIDN:CAA78556.1; PID:G31042
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:35-121/Domain: immunoglobulin homology <IMM>

Query Match 50.5%; Score 49; DB 2; Length 153;
Best Local Similarity 56.2%; Pred. No. 6.1;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFGYSYNDYYGMDV 16
DB 127 GIAGVAGTSDYYIGMDV 142

RESULT 14

H97186
glycosyltransferase domain containing protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97186
R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1044 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK0283.1; PID:GI5025335; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2327

Query Match 50.5%; Score 49; DB 2; Length 1044;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 GYSYNDYYGMDV 16
DB 143 GYGQYD--YGMDI 154

RESULT 15

S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48797
A;Molecule type: mRNA
A;Residues: 1-128 <MAH>
A;Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:G1340168
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V regions
A;Reference number: S26885; MUID:33021117; PMID:1404388
A;Accession: S26893
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 48.5; DB 2; Length 128;
Best Local Similarity 71.4%; Pred. No. 5.9;
Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 3 GYSYNDYYGMDV 16
DB 107 GYY---YYGMDV 117

Search completed: April 21, 2004, 17:38:28
Job time : 15.6087 secs

RESULT 3

S34096
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34096
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34096
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <WAG>
A:Cross-references: EMBL:X67180
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 17 RASQSVSSSYLA 28

RESULT 4

S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37520
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <KLE>
A:Cross-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405693
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 7 RASQSVSSSYLA 18

RESULT 5

S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C:Accession: S67940
R:Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A:Title: Cloning of a human autoimmune response: preparation and sequencing of a human
A:Reference number: S67940; MUID:92314301; PMID:1617110
A:Accession: S67940
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <HEX>
A:Cross-references: EMBL:X73852
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 53; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 5 RASQSVSSSYLA 16

RESULT 6

S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37513
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37513
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81362.1; PID:g405669
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 7 RASQSVSSSYLA 18

RESULT 7

S37519
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37519
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37519
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||||
DB 7 RASQSVSSSYLA 18

RESULT 8

S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37517
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501
 A:Accession: S37517
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <KLE>
 A:Cross-references: NID:g405676; PIDN:CAA81368.1; PID:g405677
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 7 RASQSVSSSYLA 18

RESULT 9

S37514
 Ig kappa chain V region (V-kappa 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37514
 R:Klein, U.; Kueppers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
 A:Reference number: S37501
 A:Accession: S37514
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <KLE>
 A:Cross-references: EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PID:g405671
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 7 RASQSVSSSYLA 18

RESULT 10

S37518
 Ig kappa chain V region (V-kappa 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37518
 R:Klein, U.; Kueppers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
 A:Reference number: S37501
 A:Accession: S37518
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <KLE>
 A:Cross-references: EMBL:Z26614; NID:g405678; PIDN:CAA81367.1; PID:g405679
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 7 RASQSVSSSYLA 18

RESULT 11

S37526
 Ig kappa chain V region (V-kappa 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
 C:Accession: S37526
 R:Klein, U.; Kueppers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
 A:Reference number: S37501
 A:Accession: S37526
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-93 <KLE>
 A:Cross-references: EMBL:Z26618; NID:g405694; PIDN:CAA81371.1; PID:g405695
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 7 RASQSVSSSYLA 18

RESULT 12

S37528
 Ig kappa chain V region (V-kappa 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37528
 R:Klein, U.; Kueppers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
 A:Reference number: S37501
 A:Accession: S37528
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-93 <KLE>
 A:Cross-references: EMBL:Z26616; NID:g405698; PIDN:CAA81369.1; PID:g405699
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 53; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 7 RASQSVSSSYLA 18

RESULT 13

A30601
 Ig kappa chain V-III region (KV325) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: A30601
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soli
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IGM autoant:
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: A30601
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-96 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0016;

Thu Apr 22 05:59:17 2004

seq4.open.rpr

Db 22 RASQSVSSSYLA 33

Search completed: April 21, 2004, 17:38:28
Job time : 10.9565 secs

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 14

K3HUNG
Ig kappa chain precursor V-III region (NG9) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 21-Jan-2000
C/Accession: A01894
R/Bentley, D.L.
Nature 307, 77-80, 1984
A/Title: Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small fa
A/Reference number: A01894; PMID:84093600; PMID:6419127
A/Accession: A01894
A/Molecule type: DNA
A/Residues: 1-100 <BEN>
A/Note: the sequence was determined from the germline gene
C/Comment: This gene was isolated from the NG9/9.1 hybridoma.
C/Genetics:
A/Gene: GDB:IGKV3
A/Cross-references: GDB:136266
A/Map position: 2p12-2p11
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; hybridoma; immunoglobulin
F/1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F/5-100/Product: Ig kappa chain V-III region (NG9) #status predicted <MAT>
F/20-95/Domain: immunoglobulin homology <IMM>
F/27-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 53; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 28 RASQSVSSSYLA 39

RESULT 15

PH0964
Ig kappa chain V region (G6+ CLL-SIC) - human (fragment)
C:Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C/Accession: PH0964
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; PMID:9202080; PMID:1552291
A/Accession: PH0964
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-104 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-21/Region: framework 1
F/14-89/Domain: immunoglobulin homology <IMM>
F/22-32/Region: complementarity-determining 1
F/33-48/Region: framework 2
F/49-54/Region: complementarity-determining 2
F/55-87/Region: framework 3
F/88-92/Region: complementarity-determining 3

Query Match 100.0%; Score 53; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 6.08696 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: SEQ4

Perfect score: 53

Sequence: 1 rasqsvsssy1a 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	100	1 KV3C_HUMAN	P01621 homo sapien
2	53	100.0	129	1 KV3L_HUMAN	P18135 homo sapien
3	53	100.0	129	1 KV3M_HUMAN	P18136 homo sapien
4	50	94.3	109	1 KV3B_HUMAN	P01620 homo sapien
5	49	92.5	109	1 KV3F_HUMAN	P01624 homo sapien
6	49	92.5	116	1 KV3J_HUMAN	P04434 homo sapien
7	46	86.8	109	1 KV3D_HUMAN	P01622 homo sapien
8	45	84.9	109	1 KV3E_HUMAN	P01623 homo sapien
9	43	81.1	108	1 KV3A_HUMAN	P01619 homo sapien
10	39	73.6	129	1 KV4A_MOUSE	P01680 mus musculu
11	38.5	72.6	115	1 KV3I_HUMAN	P04433 homo sapien
12	38	71.7	447	1 G6PI_LACLA	P81181 lactococcus
13	35	66.0	108	1 KV3V_MOUSE	P01674 mus musculu
14	35	66.0	128	1 KV3K_HUMAN	P06311 homo sapien
15	35	66.0	449	1 G6PI_STR3	Q863X1 streptococc
16	35	66.0	449	1 G6PI_STRWU	Q9X670 streptococc
17	35	66.0	449	1 G6PI_STRP3	Q8K8Q6 streptococc
18	35	66.0	449	1 G6PI_STRP8	Q9P2R3 streptococc
19	35	66.0	449	1 G6PI_STRPN	Q97N90 streptococc
20	35	66.0	449	1 G6PI_STRPY	Q9A111 streptococc
21	35	66.0	449	1 G6PI_STRP6	Q8GN74 streptococc
22	35	66.0	449	1 G6PI_STRTR	Q8VVB7 streptococc
23	35	66.0	449	1 AD02_CAVPO	G60411 cavia porce
24	35	66.0	735	1 AL16_SCHPO	P87244 schizosacch
25	34.5	65.1	108	1 KV1H_HUMAN	P01600 homo sapien
26	34	64.2	450	1 G6PI_LACFE	Q83XN3 lactobacill
27	34	64.2	450	1 G6PI_LISIN	Q928R6 listeria in
28	34	64.2	450	1 G6PI_LISNO	Q8V4R7 listeria mo
29	34	64.2	476	1 TRZA_RHOCO	Q52725 rhodococcus
30	34	64.2	782	1 ORTA_PASMU	Q9CK12 pasteurella
31	34	64.2	1177	1 Y307_MCGGE	P47549 mycoplasma
32	33	62.3	117	1 KV1J_HUMAN	P01602 homo sapien
33	33	62.3	450	1 G6PI_CLOPE	Q8X154 clostridium

```

34 33 62.3 1478 1 BUD3_ASHGO
35 32 60.4 129 1 KV3H_HUMAN
36 32 60.4 235 1 ICLN_CANFA
37 32 60.4 236 1 ICLN_MOUSE
38 32 60.4 236 1 ICLN_RAT
39 32 60.4 237 1 ICLN_HUMAN
40 32 60.4 433 1 MCRB_METEA
41 32 60.4 445 1 G6PB_BACST
42 32 60.4 474 1 ATZA_PSED
43 32 60.4 546 1 YQ44_CAEEL
44 31 58.5 111 1 KV3R_MOUSE
45 31 58.5 111 1 KV3S_MOUSE

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ALIGNMENTS

```

RESULT 1
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
a small family of germ-line V genes.";
RC Nature 307:77-80(1984).
CL -I- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; Hybridoma.
KW NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

```

Query Match 100.0%; Score 53; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 RASQSVSSSYLA 12
    |||||
DB 28 RASQSVSSSYLA 39
    |||||

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```

RESULT 2
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: The protein is one of the surface immunoglobulin M
 autoantibodies expressed in patients with chronic lymphocytic
 leukemia.
 CC PIR; PLO022; K3HUHA.
 DR HSP; P80362; IWL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 JKI SEGMENT.
 FT NON_TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14073 MW; D3C5529277774D0 CRC64;
 Query Match 100.0%; Score 53; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 0.00063;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 44 RASQSVSSSYLA 55
 RESULT 3
 KV3M_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: The protein is one of the surface immunoglobulin M
 autoantibodies expressed in patients with chronic lymphocytic
 leukemia.
 CC PIR; PLO021; K3HUHI.
 DR HSP; P80362; IWL.
 DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 JKI SEGMENT.
 FT NON_TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;
 Query Match 100.0%; Score 53; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 0.00063;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 44 RASQSVSSSYLA 55
 RESULT 4
 KV3B_HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
 Group.";
 RL Biochemistry 20:5816-5822(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 GLOBULIN ACTIVITY.
 DR PIR; A01892; K3HUSI.
 DR HSP; P80362; IWL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7699C3BCD646FFB4 CRC64;
 Query Match 94.3%; Score 50; DB 1; Length 109;
 Best Local Similarity 91.7%; Pred. No. 0.0022;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 12
 DB 44 RASQSVSSSYLA 55

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Db      24 RASQSVSSSYLA 35
RESULT 5
KV3F HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "the amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IgM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
CC PIR; A01897; K3HUPM.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT SIGNAL 1 20
FT CHAIN 21 >116
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 116
FT DISULFID 43 109
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 92.5%; Score 49; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 11
DB 44 RASQSVSSSYL 54

RESULT 7
KV3D HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";
RL Hoppe-Seyley's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUTI.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058DC7749BC CRC64;

Query Match 92.5%; Score 49; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.0036;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 24 RASQSVSSSYLA 35

RESULT 6
KV3J HUMAN
ID KV3J_HUMAN STANDARD; PRT; 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC ----- NOT_ANNOTATED_CDS.

DR EMBL; X02725; -; K3HUVH.
DR PIR; A01901; K3HUVH.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >116
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 116
FT DISULFID 43 109
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 92.5%; Score 49; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 11
DB 44 RASQSVSSSYL 54

RESULT 7
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";
RL Hoppe-Seyley's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01895; K3HUTI.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058DC7749BC CRC64;

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Query Match      86.8%; Score 46; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 24 RASQSVSNFLA 35
|||||:|:|

RESULT 8
KV3E_HUMAN          STANDARD;          PRT; 109 AA.
ID  KV3E_HUMAN
AC  P01623;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-III region WOL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=82046598; PubMed=6794615;
RA  Andrews D.W., Capra J.D.;
RT  "Amino acid sequence of the variable regions of light chains from two
RT  idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT  group."
RL  Biochemistry 20:5816-5822(1981).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC  GLOBULIN ACTIVITY.
DR  PIR; A01896; K3HUL.
DR  HSSP; P80362; LWTL.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; P:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region.
FT  DISULFID 23 89
FT  NON TER 109 109
SQ  SEQUENCE 109 AA; 11746 MW; 566C115B69CBEE CRC64;

Query Match      84.9%; Score 45; DB 1; Length 109;
Best Local Similarity 90.9%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSSYL 11
DB 24 RASQSVSSGYL 34
|||||:|:|

RESULT 9
KV3A_HUMAN          STANDARD;          PRT; 108 AA.
ID  KV3A_HUMAN
AC  P01619;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-III region B6.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RA  Milstein C.;
RT  "The basic sequences of immunoglobulin kappa chains: sequence studies
RT  of Bence Jones proteins Rad, Fr4 and B6."

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FBBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR  PIR; A01891; K3HUB6.
DR  HSSP; P80362; LWTL.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; IG_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region; Bence-Jones protein.
FT  DISULFID 23 89
FT  NON TER 108 108
SQ  SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match      81.1%; Score 43; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.063;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 24 RASQSLSGNYLA 35
|||||:|:|

RESULT 10
KV4A_MOUSE          STANDARD;          PRT; 129 AA.
ID  KV4A_MOUSE
AC  P01680;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig kappa chain V-IV region S107B precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=82115300; PubMed=6799208;
RA  Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT  "Two kappa immunoglobulin genes are expressed in the myeloma S107."
RL  Cell 26:57-66(1981).
CC  -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC  AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC  SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC  NORMAL KAPPA CHAIN S107.
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CC  -----
DR  EMBL; J00577; AAA38780.1; -.
DR  EMBL; V00780; CAA24157.1; -.
DR  PIR; A01943; KVMS7B.
DR  HSSP; P01679; 2FBJ.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; IG_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 22
FT  CHAIN 23 129
FT  DOMAIN 23 45
FT  COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 46 57
FT  COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 58 72
FT  COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 73 79
FT  COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 80 111
FT  COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 112 118
FT  DOMAIN 119 128

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FT DISULFID 45 111 BY SIMILARITY.
FT NON TER 129
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DC6BEE4 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 129;
Best Local Similarity 90.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQSVSSSYL 11
Db 47 ASSSVSSSYL 56

RESULT 11
KV31 HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC -----
DR EMBL; X01668; -; NOT ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 54 FRAMEWORK-2.
FT DOMAIN 55 69 FRAMEWORK-3.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 72.6%; Score 38.5; DB 1; Length 115;
Best Local Similarity 91.7%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSVSSSYLA 12
Db 44 RASQSV-SSSYLA 54

RESULT 12
G6PI LACLA STANDARD; PRT; 447 AA.
ID G6PI LACLA
AC P81181;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR PGIA OR LL2168
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Winkler P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
RN [2]
RP SEQUENCE OF 1-19.
RX MEDLINE=97312580; PubMed=9169021;
RX Nomura M., Nakajima I., Matsuzaki M., Kimoto H., Suzuki I., Aso H.;
RT "The N-terminal sequence of Lactococcus lactis phosphoglucose
RT isomerase purified by affinity chromatography differs from the other
RT species."
RL Arch. Biochem. Biophys. 341:315-320(1997).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate
CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GPI family.
CC -----
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CC -----
DR EMBL; AE006445; AA06266.1; -.
DR PIR; H86895; H86895.
DR HSSP; P13376; 2PGI.
DR HAMAP; MF_00473; -; 1.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT INIT MET 0
FT ACT SITE 310 310 BY SIMILARITY.
FT ACT SITE 424 424 BY SIMILARITY.
SQ SEQUENCE 447 AA; 49463 MW; 40DD4FC7D106FD29 CRC64;

Query Match 71.7%; Score 38; DB 1; Length 447;
Best Local Similarity 72.7%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQSVSSSYLA 12
Db 115 AGNSISSSYLA 125

RESULT 13
KV3V MOUSE STANDARD; PRT; 108 AA.
ID KV3V MOUSE
AC P01674;
```

DR HSSP: P01607; 1REI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;
Query Match 66.0%; Score 35; DB 1; Length 128;
Best Local Similarity 88.9%; Pred. No. 3; 6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSS 9
DB 24 RASQSVSTS 32
RESULT 14
KV3K HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III."
RL Nucleic Acids Res. 13:6495-6513 (1985).
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CC -----
CC EMBL; Z00021; CRA77316.1; -;
DR PIR; A01899; K3H041.

DR HSSP: P01607; 1REI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;
Query Match 66.0%; Score 35; DB 1; Length 128;
Best Local Similarity 88.9%; Pred. No. 3; 6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSS 9
DB 44 RASQSVSSN 52
RESULT 15
G6PI STRA3 STANDARD; PRT; 449 AA.
ID G6PI STRA3
AC Q8B6X1; Q8E1P3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR GBS0437 OR SAG0402.
OS Streptococcus agalactiae (serotype III), and
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus;
OX NCBI_TaxID=216495; 216466;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L., Meadek T., Zouine M., Couve E., Lalloui L., Poyart C., Trieu-Cuot P., Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouli H., Mulligan S., Carby H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Tachibana E.T., Brottini C., Galli G., Mariani M., Vegni F., Malone D., Rinaudo D., Rappapoli R., Telford J.L., Kasper D.L., Grandi G., Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).

```

CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the GPI family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL766845; CAD46081.1; -.
CC EMBL; AB014209; AAM99308.1; -.
CC SAGAList; gbs0437; -.
CC TIGR; SAG0402; -.
CC HAMAP; MF_00473; -.
CC InterPro; IPR001672; G6P_Isomerase.
CC Pfam; PF00342; PGI; 1.
CC PRINTS; PR00662; G6PISOMERASE.
CC PROSITE; PS00765; P_GLUCOSE_ISOMERASE 1; 1.
CC PROSITE; PS00174; P_GLUCOSE_ISOMERASE 2; 1.
CC KJ Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
CC ACT_SITE 312 312 BY SIMILARITY.
CC ACT_SITE 426 426 BY SIMILARITY.
CC SEQUENCE 449 AA; 49585 MW; 5199E72DE0CDE1B CRC64;
CC -----
Query Match 66.0%; Score 35; DB 1; Length 449;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 ASQSVSSSYLA 12
DB 117 AGNSISSTYLA 127

```

Search completed: April 21, 2004, 17:33:59
Job time : 7.08696 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 32 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ4
Perfect score: 53
Sequence: 1 rasgsvssyla 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	109	4 Q9UL86	Q9ul86 homo sapien
2	53	100.0	109	4 Q9UL78	Q9ul78 homo sapien
3	44	83.0	114	11 Q8K1F1	Q8k1f1 mus musculus
4	39	73.6	131	11 Q811C3	Q811c3 mus musculus
5	38	71.7	449	2 Q8GQP6	Q8gqp6 streptococc
6	37	69.8	363	16 Q8XKS7	Q8xks7 clostridium
7	35	66.0	101	11 Q9UL78	Q9ul78 mus musculus
8	35	66.0	108	4 Q9UL83	Q9ul83 homo sapien
9	35	66.0	124	11 Q8C3A7	Q8c3a7 mus musculus
10	35	66.0	195	2 Q8G9K4	Q8g9k4 streptococc
11	35	66.0	388	12 Q8J871	Q8j871 spodoptera
12	35	66.0	449	2 Q8SP79	Q8sp79 streptococc
13	35	66.0	449	16 Q835G1	Q835g1 enterococcu
14	35	66.0	782	4 Q96A82	Q96a82 homo sapien
15	35	66.0	1055	10 Q9SVF0	Q9svf0 arabidopsis
16	35	66.0	4753	16 Q8PLI3	Q8pli3 xanthomonas

17	34	64.2	112	17 Q9YFH8	Q9yfh8 aeropyrum p
18	34	64.2	203	10 Q65720	Q65720 arabidopsis
19	34	64.2	263	10 Q9LY95	Q9ly95 arabidopsis
20	34	64.2	276	17 Q8PZG7	Q8pzg7 methanosarc
21	34	64.2	282	10 Q8S7V3	Q8s7v3 oryza sativ
22	34	64.2	341	16 Q7UEG1	Q7ueg1 rhodospirill
23	34	64.2	384	3 Q12283	Q12283 saccharomyc
24	34	64.2	450	2 Q83XM3	Q83xm3 lactobacill
25	34	64.2	510	16 Q7UX00	Q7ux00 rhodospirill
26	34	64.2	518	13 Q42436	Q42436 notophthalm
27	34	64.2	603	3 Q9C2D7	Q9c2d7 neurospora
28	34	64.2	1465	10 Q9LQH4	Q9lqh4 arabidopsis
29	33	63.2	107	4 Q96SA9	Q96sa9 homo sapien
30	33	63.2	108	4 Q9UL77	Q9ul77 homo sapien
31	33	63.2	234	4 Q72473	Q72473 homo sapien
32	33	62.3	72	5 Q8INL7	Q8inl7 drosophila
33	33	62.3	115	6 Q9BE38	Q9be38 cryptotlagus
34	33	62.3	133	12 Q8JTH4	Q8jth4 little cher
35	33	62.3	162	13 Q9PT33	Q9pt33 oncorhynchu
36	33	62.3	174	16 Q7ULI4	Q7uli4 rhodospirill
37	33	62.3	210	8 Q8W9Q9	Q8w9q9 mesostigma
38	33	62.3	236	10 Q23193	Q23193 arabidopsis
39	33	62.3	241	17 Q96ZP0	Q96zp0 sulfolobus
40	33	62.3	309	16 Q7VA08	Q7va08 prochloroco
41	33	62.3	361	13 Q8AWC6	Q8awc6 brachydanio
42	33	62.3	475	5 Q8MPT2	Q8mpt2 caenorhabdi
43	33	62.3	487	5 Q9U2B7	Q9u2b7 caenorhabdi
44	33	62.3	510	11 Q8BUC9	Q8buc9 mus musculu
45	33	62.3	525	10 Q8LCP6	Q8lcp6 arabidopsis

ALIGNMENTS

RESULT 1
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
Query Match 100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RASQSVSSYLA 12

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Db          24 RASQSVSSSYLA 35
|||||
RESULT 2
ID Q9UL78      PRELIMINARY;      PRT;      109 AA.
AC 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
  (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96271133; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSSP; F80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5P675C52EC7EE197 CRC64;

Query Match      100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 RASQSVSSSYLA 12
Db          24 RASQSVSSSYLA 35
|||||
RESULT 3
Q8K1F1
ID Q8K1F1      PRELIMINARY;      PRT;      114 AA.
AC 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Plaque S., Katle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-VIPase response to the D-
  subunit of VIP and identification of L-VIPase VL domains.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516284; AAM64202.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match      83.0%; Score 44; DB 11; Length 114;
Best Local Similarity 90.9%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 RASQSVSSSYL 11
Db          24 RASQSVSSSYL 34
|||||
RESULT 4
Q811C3
ID Q811C3      PRELIMINARY;      PRT;      131 AA.
AC Q811C3
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MRL/MpJ-lpr/lpr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833;
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephritogenic monoclonal
  antibodies derived from an MRL/lpr lupus mouse.";
RL Mol. Immunol. 30:177-182(1993).
DR EMBL; DJ4629; BAA03482.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT CHAIN 1 22 POTENTIAL.
FT CHAIN 23 >131 IMMUNOGLOBULIN GAMMA-3 KAPPA CHAIN.
FT NON_TER 131
FT NON_TER 131
SQ SEQUENCE 131 AA; 14083 MW; 5B83656954666E9E CRC64;

Query Match      73.6%; Score 39; DB 11; Length 131;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          1 RASQSVSSSYL 11
|||||

```

Db 46 RASSVRSYYL 56

RESULT 5

Q8QOP6 PRELIMINARY; PRT; 449 AA.
 AC Q8QOP6; (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Glucose-6-phosphate isomerase.
 PGI.
 GN Streptococcus equi subsp. zooepidemicus.
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC Streptococcus.
 OC NCBI_TaxID=40041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Blank L.M., Hugenholtz P., Nielsen L.K.;
 RT "Cloning and characterization of the hyaluronic acid synthesis (has)
 RT operon from Streptococcus equi subsp. zooepidemicus.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF347022; RAN65252.1;
 DR GO; GO:0004347; F:Glucose-6-phosphate isomerase activity; IEA.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0006094; P:gluconeogenesis; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; PGI; 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 KW Isomerase.
 SQ SEQUENCE 449 AA; 49509 MW; FC23F8B6D404D96D CRC64;

Query Match 71.7%; Score 38; DB 2; Length 449;
 Best Local Similarity 72.7%; Pred No. 26;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSVSSSYLA 12

Db 117 AGNSISSSYLA 127
 |||:|||||

RESULT 6

Q8XK57 PRELIMINARY; PRT; 363 AA.
 AC Q8XK57;
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Hypothetical protein CPE1546.
 GN CPE1546.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AF003191; BAB81252.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 363 AA; 39379 MW; 791E04184ACBEDC4 CRC64;

Query Match 69.8%; Score 37; DB 16; Length 363;
 Best Local Similarity 70.0%; Pred No. 33;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQSVSSSYL 11
 :|||:|||||
 Db 81 SSQSISSSYV 90

RESULT 7

Q9JL78 PRELIMINARY; PRT; 101 AA.
 AC Q9JL78;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=A.CA;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RL with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206028; AAF69326.1; -.
 DR PIR; S17631; S17631.
 DR HSP; P01679; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 101
 SQ SEQUENCE 101 AA; 10778 MW; 0A7F6536A7E6F14D CRC64;

Query Match 66.0%; Score 35; DB 11; Length 101;
 Best Local Similarity 70.0%; Pred No. 21;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQSVSSSYL 11

Db 17 ASSSISNYL 26
 |||:|||||

RESULT 8

Q9JL83 PRELIMINARY; PRT; 108 AA.
 AC Q9JL83;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035031; AAD56267.1; -.
 DR PIR; B30609; B30609.
 DR PIR; C30609; C30609.

```

DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; IWTI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS05835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9FC5A92EBA96EEA CRC64;

Query Match 66.0%; Score 35; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSS 9
Db 24 RASQSVSSN 32

RESULT 9
Q8C3A7 PRELIMINARY; PRT; 124 AA.
AC Q8C3A7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN D930030005RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK086466; BAC39674.1; -.
DR MGD; MGI:2443927; D930030005RIK.
KW Hypothetical protein.
SQ SEQUENCE 124 AA; 13208 MW; 23EBAEBBC01083E1 CRC64;

Query Match 66.0%; Score 35; DB 11; Length 124;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 70 RGSQNSSSWLA 81

RESULT 10
Q8G9K4 PRELIMINARY; PRT; 195 AA.
AC Q8G9K4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative glucose-6-phosphate isomerase (Fragment).
GN PGI.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=G 39072;
RX MEDLINE=22269278; PubMed=12381468;
RX Sachse S., Seidel P., Gerlach D., Guenther E., Roedel J., Straube E.,
  Schmidt K.H.;
RA "Superantigen like gene(s) in human pathogenic Streptococcus
  dysgalactiae, subsp. equisimilis: Genomic localization of the gene
  encoding streptococcal pyrogenic exotoxin G (speG).";
RL FEMS Immunol. Med. Microbiol. 34:159-167(2002).
DR EMBL; AJ489606; CAD33905.1; -.
DR GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
DR GO; GO:0016853; P:isomerase activity; IEA.
DR GO; GO:0006094; P:gluconogenesis; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001672; G6P_isomerase.
DR Pfam; PF00342; PGI; 1.
FT NON_TER 195
FT NON_TER 195
SQ SEQUENCE 195 AA; 21515 MW; 52C0182D022B1F45 CRC64;

Query Match 66.0%; Score 35; DB 2; Length 195;
Best Local Similarity 63.8%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSVSSSYLA 12
Db 117 AGNSISSTYLA 127

RESULT 11
Q9J871 PRELIMINARY; PRT; 388 AA.
AC Q9J871;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ORF64.
OS Spodoptera exigua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10454;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036646; PubMed=10567663;
RX Iukel W.F.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
  Goldbach R.W., Vlak J.M.;
RA Goldbach R.W., Vlak J.M.;
RA "Sequence and organization of the spodoptera exigua multicapsid
  nucleopolyhedrovirus genome."
RT nucleopolyhedrovirus genome.
RL J. Gen. Virol. 80:3289-3304(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Iukel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
  Goldbach R.W., Vlak J.M.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169823; AAF33594.1; -.
DR InterPro; IPR008562; DUF844.
DR Pfam; PF05815; DUF844; 1.
SQ SEQUENCE 388 AA; 43654 MW; 9DDA0BCCBEC9777 CRC64;

Query Match 66.0%; Score 35; DB 12; Length 388;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 370 RASQSVSSSYNA 381

RESULT 12
Q9RP79 PRELIMINARY; PRT; 449 AA.
AC Q9RP79;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

```

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
 DE isomerase) (PFI) (Phosphohexose isomerase) (PHI).
 OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21843113; PubMed=11854208;
 RA Hughes M.J., Moore J.C., Lane J.D., Wilson R., Pribul P.K.,
 RA Younes Z.N., Dobson R.J., Everest P., Reason A.J., Redfern J.M.,
 RA Greer P.M., Paxton T., Panico M., Morris H.R., Feldman R.G.,
 RA Santangelo J.D.;
 RT "Identification of Major Outer Surface Proteins of Streptococcus
 RT agalactiae."
 RL Infect. Immun. 70:1254-1259(2002).
 CC -!- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE = D-FRUCTOSE 6-
 CC PHOSPHATE.
 CC -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
 CC EMBL; AF439651; AAL5690.1; -
 DR GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0006094; P:glucose isomerase; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; G6P; 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P-GLUCOSE-ISOMERASE_1; 1.
 DR PROSITE; PS00174; P-GLUCOSE-ISOMERASE_2; 1.
 KW Glucoseogenesis; Glycolysis; Isomerase.
 SQ SEQUENCE 449 AA; 49595 NW; 5199E72DE0CDCE1B CRC64;

Query Match 56.0%; Score 35; DB 2; Length 449;

Best Local Similarity 63.6%; Pred. No. 1.1e+02; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSVSSSYLA 12

DB 117 AGNISSTYLA 127

RESULT 13

ID Q835G1 PRELIMINARY; PRT; 449 AA.
 AC Q835G1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glucose-6-phosphate isomerase.
 GN PGI OR EF1416.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Unayam L., Brinkac L., Beanan M.,
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 RA Utterback T., Radune D., Kechum K.A., Dougherty B.A., Fraser C.M.,
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis."
 RL Science 299:2071-2074(2003).
 RL EMBL; AE016951; AAC81207.1; -
 DR TIGR; EF1416; -
 DR GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
 DR GO; GO:0016853; F:isomerase activity; IEA.

DR GO; GO:0006094; P:glucoseogenesis; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; G6P; 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P-GLUCOSE-ISOMERASE_1; 1.
 DR PROSITE; PS00174; P-GLUCOSE-ISOMERASE_2; 1.
 KW Isomerase; Complete proteome.
 SQ SEQUENCE 449 AA; 49734 NW; 1DF1A5B5D483D336 CRC64;

Query Match 66.0%; Score 35; DB 16; Length 449;

Best Local Similarity 63.6%; Pred. No. 1.1e+02; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSVSSSYLA 12

DB 116 AGNISSTYLA 126

RESULT 14

ID Q96A82 PRELIMINARY; PRT; 782 AA.
 AC Q96A82;
 DT 01-DEC-2001 (TrEMBLrel. 13, Created)
 DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ30106 (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Kikuchi K., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project."
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK054668; BAB70788.1; -
 DR InterPro; IPR007421; DUF467.
 DR Pfam; PF04326; AAA_div; 1.
 KW Hypothetical protein.
 FT NON TER 782 782
 SQ SEQUENCE 782 AA; 89004 MW; 7BA657A17714028B CRC64;

Query Match 56.0%; Score 35; DB 4; Length 782;

Best Local Similarity 72.7%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11

DB 501 RKAQSVSSYL 511

RESULT 15

ID Q9SVF0 PRELIMINARY; PRT; 1055 AA.
 AC Q9SVF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F2113.110 OR A14G38350.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Schueller C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A.
 RA Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035539; CAB37491.1; -;
 DR EMBL; AL161593; CAB80500.1; -;
 DR PIR; T05663; T05663.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008158; F:heghehog receptor activity; IEA.
 DR GO; GO:0030301; P:cholesterol transport; IEA.
 DR InterPro; IPR004765; NP_C type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD 5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS50156; SSD; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1055 AA; 116148 MW; 15E154A61DC936BC CRC64;

Query Match 66.0%; Score 35; DB 10; Length 1055;
 Best Local Similarity 58.3%; Pred. No. 2.8e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 DB 778 RASQASDTSYIA 789

Search completed: April 21, 2004, 17:37:18
 Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 48 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ4

Perfect score: 53

Sequence: 1 rasqsvassyla 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	12	AA15375	AA15375 Igm-RF G1
2	53	100.0	12	AAU70331	AAU70331 Human Kap
3	53	100.0	12	AAU83718	AAU83718 MS-GPC-6
4	53	100.0	12	ABB57480	ABB57480 HLA-DR-sp
5	53	100.0	12	ABB57475	ABB57475 HLA-DR-sp
6	53	100.0	12	ABB57469	ABB57469 HLA-DR-sp
7	53	100.0	12	ABB57472	ABB57472 HLA-DR-sp
8	53	100.0	12	AAE38096	AAE38096 Human COU
9	53	100.0	12	AAE38067	AAE38067 Human 17G
10	53	100.0	12	AAE38067	AAE38067 Human 17G
11	53	100.0	12	ADA90302	ADA90302 MS-Roch
12	53	100.0	12	ADA90308	ADA90308 MS-Roch
13	53	100.0	12	ADA90317	ADA90317 MS-Roch
14	53	100.0	12	ADA90323	ADA90323 MS-Roch
15	53	100.0	12	ADA90324	ADA90324 MS-Roch
16	53	100.0	12	ADA90641	ADA90641 MS-Roch
17	53	100.0	12	ADA90751	ADA90751 MS-Roch
18	53	100.0	12	ADA90867	ADA90867 MS-Roch
19	53	100.0	12	ADA90869	ADA90869 MS-Roch
20	53	100.0	12	ADA91097	ADA91097 MS-R Fab/
21	53	100.0	12	ADA90322	ADA90322 MS-Roch
22	53	100.0	12	ADA90487	ADA90487 MS-Roch
23	53	100.0	12	ADA90497	ADA90497 MS-Roch
24	53	100.0	12	ADA90871	ADA90871 MS-Roch
25	53	100.0	12	ADA90953	ADA90953 MS-R Fab/
				ADA91010	ADA91010 MS-R Fab/

26	53	100.0	12	6	ADA91235	ADA91235 MS-R Fab/
27	53	100.0	12	6	ADA91241	ADA91241 MS-R Fab/
28	53	100.0	12	6	ADA90301	ADA90301 MS-Roch
29	53	100.0	12	6	ADA90309	ADA90309 MS-Roch
30	53	100.0	12	6	ADA90488	ADA90488 MS-Roch
31	53	100.0	12	6	ADA90637	ADA90637 MS-Roch
32	53	100.0	12	6	ADA90756	ADA90756 MS-Roch
33	53	100.0	12	6	ADA90313	ADA90313 MS-Roch
34	53	100.0	12	6	ADA90320	ADA90320 MS-Roch
35	53	100.0	12	6	ADA90484	ADA90484 MS-Roch
36	53	100.0	12	6	ADA90490	ADA90490 MS-Roch
37	53	100.0	12	6	ADA90631	ADA90631 MS-Roch
38	53	100.0	12	6	ADA90643	ADA90643 MS-Roch
39	53	100.0	12	6	ADA90989	ADA90989 MS-R Fab/
40	53	100.0	12	6	ADA91339	ADA91339 MS-R Fab/
41	53	100.0	12	6	ADA90315	ADA90315 MS-Roch
42	53	100.0	12	6	ADA90321	ADA90321 MS-Roch
43	53	100.0	12	6	ADA90325	ADA90325 MS-Roch
44	53	100.0	12	6	ADA90479	ADA90479 MS-Roch
45	53	100.0	12	6	ADA90495	ADA90495 MS-Roch

ALIGNMENTS

RESULT 1
AA15375
ID AA15375 standard; protein; 12 AA.

XX AA15375;

DT 25-MAR-2003 (revised)

DT 05-MAR-1992 (first entry)

XX Igm-RF Glo.

XX Rheumatoid factor; RF; antigen; CDR; Igm.

XX Synthetic.

XX US068177-A.

XX 26-NOV-1991.

XX 05-AUG-1985; 85US-00762698.

XX 05-AUG-1985; 85US-00762698.

XX (SCRI) SCRIPPS CLINIC & RES FOUND.

XX Carson DA, Fong S, Chen PP;

XX WFI; 1991-368612/50.

XX Synthetic polypeptide(s) for inducing anti-idiotypic antibodies - useful for treating auto immune-, endocrine- and rheumatic-diseases and myasthenia gravis.

XX Claim 10; Page 42; 44pp; English.

XX Three rabbits were inoculated with two s.c. injections of PGL1 (synthetic peptide) conjugated to KLH as an immunogen, and their sera were analysed for anti-peptide antibody activity by ELISA. All three immunised rabbits produced anti-PGL1 antibody. Antisera drawn from a rabbit on two different days reacted significantly with the corresp. intact Igm-RF Glo. See also AA15365-74 and AA15375. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 1 RASQSVSSSYLA 12

RESULT 2

AAU70331
 ID AAU70331 standard; peptide; 12 AA.
 AC AAU70331;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Kappa III light chain CDR1.
 XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgW; kappa; lambda; CHBP.
 XX
 OS Homo sapiens.
 XX
 PN WO200183806-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014349.
 XX
 PR 02-MAY-2000; 2000US-00563222.
 XX
 PA (EPIC-) EPICYTE PHARM INC.
 XX
 PI Hiatt AC, Hein MB;
 XX
 DR WPI; 2002-055482/07.
 XX
 PT Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 PS Disclosure; Page 14; 129pp; English.

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention

Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. NO. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
 |||||
 Db 1 RASQSVSSSYLA 12

RESULT 3

AAU83718
 ID AAU83718 standard; peptide; 12 AA.
 XX
 AC AAU83718;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE MS-GPC-6 light chain variable region CD1 sequence.
 XX
 KW Human; antibody-based antigen; HLA-DR; CDR; antibody;
 KW human leukocyte antigen; cell proliferative disorder; lymphoma;
 KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
 KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
 KW Grave's disease; insulin-dependent diabetes; transplant rejection;
 KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
 KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
 KW IL-2; MS-GPC; complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 PN WO200187337-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US015625.
 XX
 PR 12-MAY-2000; 2000EP-00110065.
 PR 06-OCT-2000; 2000US-0238492P.
 XX
 PA (GPCB-) GPC BIOTECH AG.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
 XX
 DR WPI; 2002-075288/10.
 XX
 PT Polypeptide compositions which bind to cell surface epitopes, which in
 PT multivalent form kills lymphoid tumor cells and in monovalent form causes
 PT immunosuppression or inhibits activation of lymphocytes.
 XX
 PS Example 4; Page 66; 150pp; English.

The invention relates to a composition which includes a polypeptide or a multivalent polypeptide comprising one or more antibody-based antigen - binding domain of human composition with binding specificity for an antigen expressed on surface of a human cell, especially HLA-DR (human leukocyte antigen DR), where treating cells expressing HLA-DR with the multivalent polypeptide causes or leads to killing of cells without need of cytotoxic entities or immunological mechanisms. Also included are the nucleic acid encoding the polypeptide, a vector comprising the nucleic acid and a host cell harbouring vector or nucleic acid. The polypeptide (optionally linked to cytotoxic or immunogenic agent), the nucleic acid and the host cell are useful for preparing a pharmaceutical preparation for the treatment of cell proliferative disorders, disorders involving transformed cells expressing MHC class II antigens, B cell non-Hodgkin's lymphoma, B cell lymphoma, B cell acute lymphoid leukaemia, Burkitt's lymphoma, Hodgkin's lymphoma, hairy cell leukaemia, acute myeloid leukaemia, T cell lymphoma, T cell non-Hodgkin's lymphoma, chronic myeloid leukaemia, chronic lymphoid leukaemia or multiple myeloid leukaemia, disorders involving unwanted activation of the cells of the immune system, such as lymphoid cells expressing MHC class II, rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft vs. host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. The antigen is useful for suppressing activation or proliferation of a cell of the immune system, suppressing interleukin-2 (IL-2) secretion by a cell of the immune system, such as expressing HLA-DR, the interaction of the cell of the immune system with another cell, immunosuppressing a patient and for killing a cell expressing an antigen, HLA-DR on the surface of the cell, where neither cytotoxic entities nor immunological

XX Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
XX
XX Example; Page 60; 139pp; English.
XX
XX The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microM or less. (I) has
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatologic, and
CC antithyroid, nephrotropic, thymimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
CC the exemplification of the present invention
XX
XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12
RESULT 6
ABB57469
ID ABB57469 standard; peptide; 12 AA.
XX
XX ABB57469;
XX
XX 18-MAR-2002 (first entry)
XX
XX HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-2.

XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
XX human leukocyte antigen; immune system; immunosuppression; antibody;
XX major histocompatibility complex; antirheumatic; antiarthritic;
XX neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
XX immunosuppressive; dermatologic; antithyroid; nephrotropic; psoriasis;
XX thymimetic; hepatotropic; immune response suppressor; narcolepsy;
XX rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
XX Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
XX systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
XX transplant rejection; graft versus host disease; pemphigus vulgaris;
XX glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
XX irritable bowel disease; Sjogren's syndrome.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200187338-A1.

22-NOV-2001.
14-MAY-2001; 2001WO-US015626.
12-MAY-2000; 2000EP-00110063.
06-OCT-2000; 2000US-0238762P.
(GPCB-) GPC BIOTECH AG.
(MORP-) MORPHOSYS AG.
Nagy Z, Tesar M, Thomassen-Wolf E;
WPI; 2002-075289/10.
Composition for suppressing immune response, treating diseases of immune
system, has polypeptide comprising antibody-based antigen-binding domain
of human composition, which binds antigen expressed on a cell surface.
Example; Page 60; 139pp; English.
The present invention describes a composition (I), comprising a
polypeptide comprising an antibody-based antigen-binding domain of human
composition with binding specificity for an antigen expressed on the
surface of a cell, where treating cells expressing the antigen with the
polypeptides leads to suppression of an immune response, and the IC50 for
the suppression of immune response is 1 microM or less. (I) has
antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
antidiabetic, antipsoriatic, immunosuppressive, dermatologic, and
antithyroid, nephrotropic, thymimetic and hepatotropic activities, and
can be used as a suppressor of immune response. (I) is useful for
suppressing activation or proliferation of a cell of the immune system,
suppressing IL-2 secretion by a cell, the interaction of a cell of the
immune system with another cell, immunosuppressing a patient and for
killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
the surface of the cell, where neither cytotoxic entities nor
immunological mechanisms are needed to cause or lead to the killing. (I)
(optionally linked to cytotoxic or immunogenic agent) is useful for
preparing a pharmaceutical preparation for the treatment of rheumatoid
arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
erythematosus, ankylosing spondylitis, transplant rejection, graft versus
host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
the exemplification of the present invention
XX
XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12
RESULT 7
ABB57472
ID ABB57472 standard; peptide; 12 AA.
XX
XX ABB57472;
XX
XX 18-MAR-2002 (first entry)
XX
XX HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-3.
XX
XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
XX human leukocyte antigen; immune system; immunosuppression; antibody;
XX major histocompatibility complex; antirheumatic; antiarthritic;
XX neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
XX immunosuppressive; dermatologic; antithyroid; nephrotropic; psoriasis;
XX thymimetic; hepatotropic; immune response suppressor; narcolepsy;
XX rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
XX Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
XX systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
XX transplant rejection; graft versus host disease; pemphigus vulgaris;
XX glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
XX irritable bowel disease; Sjogren's syndrome.

KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;
KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
KW transplant rejection; graft versus host disease; pemphigus vulgaris;
KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
KW irritable bowel disease; Sjogren's syndrome.
XX
XX Homo sapiens.
OS Synthetic.
XX WO200187338-A1.
PN
PD 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015626.
PF
XX 12-MAY-2000; 2000EP-00110063.
PR
XX 06-OCT-2000; 2000US-0238762P.
XX
XX (GPCB-) GPC BIOTECH AG.
PA
XX (MORP-) MORPHOSYS AG.
XX
XX Nagy Z, Tesar M, Thomassen-Wolf E;
PI
XX WPI; 2002-075289/10.
DR
XX
XX Composition for suppressing immune response, treating diseases of immune
PT system, has polypeptide comprising antibody-based antigen-binding domain
PT of human composition, which binds antigen expressed on a cell surface.
XX
XX Example; Page 60; 139pp; English.
XX
XX The present invention describes a composition (I), comprising a
CC polypeptide comprising an antibody-based antigen-binding domain of human
CC composition with binding specificity for an antigen expressed on the
CC surface of a cell, where treating cells expressing the antigen with the
CC polypeptides leads to suppression of an immune response, and the IC50 for
CC the suppression of immune response is 1 microm or less. (I) has
CC antiheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,
CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and
CC can be used as a suppressor of immune response. (I) is useful for
CC suppressing activation or proliferation of a cell of the immune system,
CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
CC immune system with another cell, immunosuppressing a patient and for
CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR on
CC the surface of the cell, where neither cytotoxic entities nor
CC immunological mechanisms are needed to cause or lead to the killing. (I)
CC (optionally linked to cytotoxic or immunogenic agent) is useful for
CC preparing a pharmaceutical preparation for the treatment of rheumatoid
CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
XX the exemplification of the present invention
XX
XX Sequence 12 AA;

Query Match 100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
|||
Db 1 RASQSVSSSYLA 12

RESULT 8
AAE38096

ID AAE38096 standard; peptide; 12 AA.
XX
AC AAE38096;
XX
XX 06-NOV-2003 (first entry)
DT
XX Human COU-1 antibody VL CDR1 peptide #1.
DE
XX
XX Human; cancer-associated epitope; cytochrome K8; cytochrome K18; VL;
KW adenocarcinoma; therapy; cancer; antibody; light chain variable region;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO2003057168-A2.
PN
XX 17-JUL-2003.
PD
XX
XX 03-JAN-2003; 2003WO-US000297.
PF
XX
XX 03-JAN-2002; 2002US-0345208P.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Ditzel H, Jensenius JC;
PI
XX WPI; 2003-598315/56.
DR
XX
XX Novel isolated cancer-associated epitope comprising two separate
PT polypeptides, a cytochrome K8 polypeptide and a cytochrome K18
PT polypeptide, useful as component of vaccine for preventing or treating
PT adenocarcinoma.
XX
XX Claim 15; Page 36; 155pp; English.
XX
XX The invention provides a cancer-associated epitope comprising two
CC separate polypeptides, a cytochrome K8 polypeptide and a cytochrome K18
CC polypeptide. Vaccine composition of the invention is useful for treating
CC or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
CC adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
CC adenocarcinoma or non-seminoma testis carcinoma. The invention is also
CC useful for preparing a medicament for treating or preventing cancer in a
CC mammal. The present sequence is human COU-1 cancer-associated epitope
CC antibody VL (light chain variable region) CDR (complementarity
CC determining region) peptide
XX
XX Sequence 12 AA;
SQ
Query Match 100.0%; Score 53; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 12
|||
Db 1 RASQSVSSSYLA 12
RESULT 9
AAE38067
ID AAE38067 standard; peptide; 12 AA.
XX
AC AAE38067;
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human 17G1 CD30 antibody VL CDR1 peptide.
DE
XX
XX Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; Grave's disease; AICL;
KW atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
KW acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
KW Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
KW adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;
KW

KW Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
 KW light chain variable domain; VL; complementarity determining region; CDR.
 OS Homo sapiens.
 XX WO2003059282-A2.
 XX PD 24-JUL-2003.
 XX 07-JAN-2003; 2003WO-US000440.
 XX 09-JAN-2002; 2002US-0347649P.
 XX 19-AUG-2002; 2002US-0404427P.
 XX 06-DEC-2002; 2002US-0431684P.
 XX (MEDA-) MEDAREX INC.
 XX Keler T, Graziano R, Trembl J;
 XX WPI: 2003-598476/56.
 XX N-FSDS; AAD57379.
 XX New human monoclonal antibody that binds to human CD30, useful for
 PT treating or preventing tumor or autoimmune disease, e.g., rheumatoid
 PT arthritis.
 XX Disclosure; Page 117; 122pp; English.
 XX The invention relates to human monoclonal antibody that binds to human
 XX CD30. The antibody is useful for treating or preventing tumor or
 CC autoimmune disease e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
 CC Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,
 CC chronic renal failure, acute infectious mononucleosis, herpes or HIV
 CC (human immunodeficiency virus) virus-associated diseases. The antibody is
 CC also useful for treating Hodgkin's disease, anaplastic large cell
 CC lymphoma (ALCL), adult T cell lymphoma, HIV associated body cavity
 CC lymphadenopathy (AILD)-like T cell lymphoma, undifferentiated carcinomas of the
 CC based lymphomas, embryonal carcinomas, Castleman's disease, Kaposi's
 CC rhino-pharynx (e.g. Schinckel's tumour), Castleman's disease, Kaposi's
 CC Sarcoma and other T-cell or B-cell lymphomas. The present sequence is
 CC human CD30 antibody VL (light chain variable domain) CDR (complementarity
 CC determining region) peptide
 XX Sequence 12 AA;
 XX Query Match 100.0%; Score 53; DB 6; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 0.0013;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSSYLA 12
 Db |||||
 1 RASQSVSSSYLA 12
 RESULT 10
 ADA90302
 ID ADA90302 standard; peptide; 12 AA.
 XX AC ADA90302;
 XX AC
 XX 20-NOV-2003 (first entry)
 XX DE MS-Roche #3.2 L-CDR1 amino acid sequence.
 XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW nontropic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
 KW neuronal disorder; aging.

OS Synthetic.
 OS Homo sapiens.
 XX WO2003070760-A2.
 XX PD 28-AUG-2003.
 XX 20-FEB-2003; 2003WO-BP001759.
 XX 20-FEB-2002; 2002EP-00003844.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX (MORP-) MORPHOSYS AG.
 XX Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;
 XX Loehning C, Loetscher H, Nordstedt C, Rothe C;
 XX WPI: 2003-663848/62.
 XX New antibody molecule capable of specifically recognizing two regions of
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 PT diseases associated with amyloidogenesis or amyloid-plaque formation
 PT (e.g. dementia).
 XX Example 5; Page 64; 312pp; English.
 XX The present invention describes an antibody molecule (I) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA98986 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA98987 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (I), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (I) and recovering (I) from the culture; (5) a composition comprising (I)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (I),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (I); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
 CC composition, comprising optimisation of (I), and formulating the
 CC pharmaceutical composition prepared by method (8). (I) has
 CC neuroprotective, nontropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC disintegration of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.
 XX Sequence 12 AA;
 XX Query Match 100.0%; Score 53; DB 6; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 0.0013;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSSYLA 12
 Db |||||
 1 RASQSVSSSYLA 12
 RESULT 11
 ADA90308
 ID ADA90308 standard; peptide; 12 AA.

pharmaceutical composition prepared by method (8). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disinization of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

Sequence 12 AA;

Query Match 100.0%; Score 53; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 RASQSVSSSYLA 12
 |||||
 DDB 1 RASQSVSSSYLA 12

RESULT 13
 ADA90323
 ID ADA90323 standard; peptide; 12 AA.
 AC
 AC ADA90323;
 DT 20-NOV-2003 (first entry)
 XX MS-Roche #3.4.H12 L-CDRI amino acid sequence.
 DE
 XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW nootropic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
 KW neuronal disorder; aging.
 XX Synthetic.
 XX Homo sapiens.
 XX
 XX WO2003070760-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 20-FEB-2003; 2003WO-EP001759.
 XX PF
 XX 20-FEB-2002; 2002EP-00003844.
 XX PR
 XX (HOPF) HOFFMANN LA ROCHE & CO AG F.
 XX PA (MORP-) MORPHOSYS AG.
 XX PA
 XX Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;
 PI Loelning C, Loetscher H, Nordstedt C, Rothe C;
 PI
 XX WPI; 2003-663848/62.
 XX DR
 XX New antibody molecule capable of specifically recognizing two regions of
 PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 PT diseases associated with amyloidogenesis or amyloid-plaque formation
 PT (e.g. dementia).
 XX
 XX Example 5; Page 64; 312pp; English.
 XX
 XX The present invention describes an antibody molecule (I) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The

CC	first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC	Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the
CC	amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-
CC	Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule
CC	encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
CC	cell comprising the vector of (2); (4) preparing (1), comprising
CC	culturing the host cell of (3) under conditions that allow synthesis of
CC	(1) and recovering (1) from the culture; (5) a composition comprising (1)
CC	or an antibody molecule produced by method (4); (6) a kit comprising (1),
CC	nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC	(1); (8) testing the resulting Fab optimisation library by panning
CC	against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
CC	of selected, optimised clones; (11) preparing a pharmaceutical
CC	composition, optimised clones; (12) preparing a pharmaceutical
CC	optimised antibody/antibody molecule with a carrier; and (12) a
CC	pharmaceutical composition prepared by method (8). (1) has
CC	neuroprotective, neurotropic and antiparkinsonian activities, and can be
CC	used in gene therapy. The antibody molecule (1), nucleic acid molecule,
CC	vector or host is useful in preparing a pharmaceutical composition for
CC	the prevention and/or treatment of a disease associated with
CC	amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC	may also be used in preparing a diagnostic composition for the detection
CC	of the disease mentioned above. The antibody is used for the
CC	dissociation of beta-amyloid plaques or for passive immunisation
CC	against beta-amyloid plaque formation. In particular, the disease is
CC	dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
CC	Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
CC	amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
CC	amyotrophic lateral sclerosis or neuronal disorders related to aging. The
CC	present sequence is used in the exemplification of the present invention.
XX	
SS	Sequence 12 AA;
QY	Query Match 100.0%; Score 53; DB 6; Length 12;
DB	Best Local Similarity 100.0%, Fred. No. 0.0013;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RASQSVSSSYLA 12
DB	
	1 RASQSVSSSYLA 12
RESULT 14	
ID	ADA90324
XX	ADA90324 standard; peptide; 12 AA.
AC	ADA90324;
DT	20-NOV-2003 (first entry)
DE	MS-Roche #3.4.H13 L-CDR1 amino acid sequence.
XX	antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
XX	neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW	amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW	Alzheimer's disease; motor neuropathy; Down's syndrome;
KW	Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW	Parkinson's disease; HIV-related dementia; amytrophic lateral sclerosis;
XX	neuronal disorder; aging.
OS	Synthetic.
OS	Homo sapiens.
FN	WC2003070760-A2.
XX	28-AUG-2003.
PD	
PF	20-FEB-2003; 2003WO-EP001759.
XX	
PR	20-FEB-2002; 2002EP-00003844.
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
PA	(NORP-) MORPHOSYS AG.

XX FI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
 XX PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
 XX XX WPI; 2003-663848/62.
 XX DR
 XX PT New antibody molecule capable of specifically recognizing two regions of
 XX PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 XX PT diseases associated with amyloidogenesis or amyloid-plaque formation
 XX PT (e.g. dementia).
 XX XX
 XX PS Example 5; Page 64; 312pp; English.
 XX XX
 CC The present invention describes an antibody molecule (I) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (1), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (1); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
 CC of selected, optimised clones; (11) preparing a pharmaceutical
 CC composition, comprising optimisation of (1), and formulating the
 CC optimised antibody/antibody molecule with a carrier; and (12) a
 CC pharmaceutical composition prepared by method (8). (1) has
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC disintegration of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.
 XX SQ Sequence 12 AA;
 Query Match 100.0%; Score 53; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. NO. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSSYLA 12
 Db 1 RASQSVSSSYLA 12
 RESULT 15
 ADA90641
 ID ADA90641 standard; peptide; 12 AA.
 AC ADA90641;
 XX AC
 XX DT 20-NOV-2003 (first entry)
 XX XX
 XX DE MS-Roche #7.9.H1 L-CDR1 amino acid sequence.
 XX XX
 XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
 KW neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

KW neuronal disorder; aging.
 XX Synthetic.
 OS Homo sapiens.
 XX XX
 XX PN WO2003070760-A2.
 XX XX
 XX PD 28-AUG-2003.
 XX XX
 XX PF 20-FEB-2003; 2003WO-EF001759.
 XX XX
 XX PR 20-FEB-2002; 2002EP-00003844.
 XX XX
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PA (MORP-) MORPHOSYS AG.
 XX XX
 XX PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T;
 XX PI Loehning C, Loetscher H, Nordstedt C, Rothe C;
 XX XX WPI; 2003-663848/62.
 XX DR
 XX XX
 XX PT New antibody molecule capable of specifically recognizing two regions of
 XX PT the beta-A4 peptide, useful for diagnosing, preventing or treating
 XX PT diseases associated with amyloidogenesis or amyloid-plaque formation
 XX PT (e.g. dementia).
 XX XX
 XX PS Example 5; Page 66; 312pp; English.
 XX XX
 CC The present invention describes an antibody molecule (I) capable of
 CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
 CC Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
 CC Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
 CC cell comprising the vector of (2); (4) preparing (1), comprising
 CC culturing the host cell of (3) under conditions that allow synthesis of
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
 CC (1); (8) testing the resulting Fab optimisation library by panning
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
 CC of selected, optimised clones; (11) preparing a pharmaceutical
 CC composition, comprising optimisation of (1), and formulating the
 CC optimised antibody/antibody molecule with a carrier; and (12) a
 CC pharmaceutical composition prepared by method (8). (1) has
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
 CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
 CC vector or host is useful in preparing a pharmaceutical composition for
 CC the prevention and/or treatment of a disease associated with
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
 CC may also be used in preparing a diagnostic composition for the detection
 CC of the disease mentioned above. The antibody is used for the
 CC disintegration of beta-amyloid plaques or for passive immunisation
 CC against beta-amyloid plaque formation. In particular, the disease is
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The
 CC present sequence is used in the exemplification of the present invention.
 XX SQ Sequence 12 AA;
 Query Match 100.0%; Score 53; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. NO. 0.0013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSSYLA 12
 Db 1 RASQSVSSSYLA 12

Search completed: April 21, 2004, 17:33:12

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:33:24 ; Search time 178.435 Seconds
(without alignments)
65.641 Million cell updates/sec

Title: SEQ4
Perfect score: 53
Sequence: 1 rasqvssysla 12

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 97603577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

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5:	/cgn2_6/ptodata/2/paa/US08 COMB.pcp.*
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33:	/cgn2_6/ptodata/2/paa/US08 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	100.0	12	US01-14349-11	Sequence 11, Appl
2	100.0	100.0	12	US02-10788-38	Sequence 38, Appl
3	100.0	100.0	12	US02-10788-40	Sequence 40, Appl
4	100.0	100.0	12	US02-10788-41	Sequence 41, Appl
5	100.0	100.0	12	US02-10788-42	Sequence 42, Appl
6	100.0	100.0	12	US03-00297-15	Sequence 15, Appl
7	100.0	100.0	12	US03-00440-20	Sequence 20, Appl
8	100.0	100.0	12	US03-06155-4	Sequence 4, Appl
9	100.0	100.0	12	US03-32678-38	Sequence 38, Appl
10	100.0	100.0	12	US03-32871-38	Sequence 38, Appl
11	100.0	100.0	12	US03-36126-38	Sequence 38, Appl
12	100.0	100.0	12	US03-38234-194	Sequence 194, App
13	100.0	100.0	12	US98-24303-124	Sequence 124, App
14	100.0	100.0	12	US-09-191-817-124	Sequence 124, App
15	100.0	100.0	12	US-09-563-222-11	Sequence 11, Appl
16	100.0	100.0	12	US-09-563-222C-11	Sequence 11, Appl
17	100.0	100.0	12	US-09-828-708-38	Sequence 38, Appl
18	100.0	100.0	12	US-09-828-708-40	Sequence 40, Appl
19	100.0	100.0	12	US-09-828-708-41	Sequence 41, Appl
20	100.0	100.0	12	US-09-828-708-42	Sequence 42, Appl
21	100.0	100.0	12	US-10-001-934-62	Sequence 62, Appl
22	100.0	100.0	12	US-10-275-046-19	Sequence 19, Appl
23	100.0	100.0	12	US-10-338-366-20	Sequence 20, Appl
24	100.0	100.0	12	US-10-374-932-8	Sequence 8, Appl
25	100.0	100.0	12	US-10-379-741-8	Sequence 8, Appl
26	100.0	100.0	12	US-10-684-957-38	Sequence 38, Appl
27	100.0	100.0	12	US-10-714-353-38	Sequence 38, Appl
28	100.0	100.0	12	US-10-726-332-194	Sequence 194, App
29	100.0	100.0	12	PCT-US03-32243-68	Sequence 68, Appl
30	100.0	100.0	28	US-10-269-711-57	Sequence 57, Appl
31	100.0	100.0	28	US-10-684-109-68	Sequence 68, Appl
32	100.0	100.0	28	US-60-418-031-57	Sequence 57, Appl
33	100.0	100.0	66	US-60-196-718-5772	Sequence 5772, Ap
34	100.0	100.0	74	PCT-US02-12202-23	Sequence 23, Appl
35	100.0	100.0	74	US-10-125-687-23	Sequence 23, Appl
36	100.0	100.0	80	US-09-791-537-35418	Sequence 35418, A
37	100.0	100.0	80	US-09-791-537-36133	Sequence 36133, A
38	100.0	100.0	81	US-09-791-537-35334	Sequence 35334, A
39	100.0	100.0	81	US-09-791-537-35348	Sequence 35348, A
40	100.0	100.0	81	US-09-791-537-35453	Sequence 35453, A
41	100.0	100.0	81	US-09-791-537-35493	Sequence 35493, A
42	100.0	100.0	81	US-09-791-537-36105	Sequence 36105, A
43	100.0	100.0	81	US-09-791-537-36107	Sequence 36107, A
44	100.0	100.0	81	US-09-791-537-36163	Sequence 36163, A
45	100.0	100.0	81	US-09-791-537-36683	Sequence 36683, A

Query Match 100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1
PCT-US01-14349-11
; Sequence 11, Application PC/TUS0114349
; GENERAL INFORMATION:
; APPLICANT: EpiCyte Pharmaceuticals, Inc.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Heintz, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406PC
; CURRENT APPLICATION NUMBER: PCT/US01/14349
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US01-14349-11

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QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 2
PCT-US02-10788-38
; Sequence 38, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-38

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 3
PCT-US02-10788-40
; Sequence 40, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-40

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 4
PCT-US02-10788-41
; Sequence 41, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-41

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 5
PCT-US02-10788-42
; Sequence 42, Application PC/TUS0210788
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
; FILE REFERENCE: 1361.005W01
; CURRENT APPLICATION NUMBER: PCT/US02/10788
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10788-42

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 6
PCT-US03-00297-15
; Sequence 15, Application PC/TUS0300297
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017W01
; CURRENT APPLICATION NUMBER: PCT/US03/00297
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15

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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-00297-15

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 7
PCT-US03-00440-20
; Sequence 20, Application PC/TUS0300440
; GENERAL INFORMATION:
; APPLICANT: Medarex, Inc. et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180PC
; CURRENT APPLICATION NUMBER: PCT/US03/00440
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-00440-20

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 8
PCT-US03-06155-4
; Sequence 4, Application PC/TUS0306155
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Antagonistic Anti-rFas Ligand Human Antibodies and Fragments Thereof
; FILE REFERENCE: X15450
; CURRENT APPLICATION NUMBER: PCT/US03/06155
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-06155-4

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 9
PCT-US03-32678-38
; Sequence 38, Application PC/TUS0332678
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamma
; FILE REFERENCE: 01-1635-G
; CURRENT APPLICATION NUMBER: PCT/US03/32678
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-32678-38

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 10
PCT-US03-32871-38
; Sequence 38, Application PC/TUS0332871
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; APPLICANT: Medarex, Inc.
; APPLICANT: Welcher, Andrew
; APPLICANT: Chute, Hilary
; APPLICANT: Li, Luke
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamma
; FILE REFERENCE: 01-1635-G
; CURRENT APPLICATION NUMBER: PCT/US03/32871
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 60/419,057
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/479,241
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-32871-38

Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 12
Db      1 RASQSVSSSYLA 12

RESULT 11
PCT-US03-36126-38
; Sequence 38, Application PC/TUS0336126

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; GENERAL INFORMATION:
; APPLICANT: Genmab A/S
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
; FILE REFERENCE: GMI-059PC
; CURRENT APPLICATION NUMBER: PCT/US03/36126
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426690
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-36126-38

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Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RASQSVSSSYLA 12
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Db      1 RASQSVSSSYLA 12

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RESULT 12
PCT-US03-38234-194
; Sequence 194, Application PC/TUS0338234
; GENERAL INFORMATION:
; APPLICANT: Abgenix, Inc.
; APPLICANT: Lexicon Genetics Incorporated
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: PCT/US03/38234
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234-194

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Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RASQSVSSSYLA 12
      |||||
Db      1 RASQSVSSSYLA 12

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RESULT 13
PCT-US98-24303-124
; Sequence 124, Application PC/TUS9824303
; GENERAL INFORMATION:
; APPLICANT: Purdue Pharma L.P.
; TITLE OF INVENTION: MODIFIED ANTIBODIES WITH ENHANCED ABILITY TO ELICIT AN
; FILE REFERENCE: 6750-015-228
; CURRENT APPLICATION NUMBER: PCT/US98/24303
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/081,403

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; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/065,716
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-24303-124

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Query Match      100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 RASQSVSSSYLA 12
      |||||
Db      1 RASQSVSSSYLA 12

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RESULT 14
US-09-191-817-124
; Sequence 124, Application US/09191817
; GENERAL INFORMATION:
; APPLICANT: Burch, R.M.
; TITLE OF INVENTION: MODIFIED ANTIBODIES WITH ENHANCED ABILITY TO ELICIT AN
; FILE REFERENCE: 6750-015
; CURRENT APPLICATION NUMBER: US/09/191,817
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/081,403
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/065,716
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-191-817-124

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Db      1 RASQSVSSSYLA 12

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RESULT 15
US-09-563-222-11
; Sequence 11, Application US/09563222
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-11

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Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

Search completed: April 21, 2004, 17:57:23
Job time : 179.435 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 36.1739 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ4

Perfect score: 53

Sequence: 1 RASQSVSSSYLA 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	53	100.0	12	9 US-09-828-708-40	Sequence 40, Appl
3	53	100.0	12	9 US-09-828-708-41	Sequence 41, Appl
4	53	100.0	12	9 US-09-828-708-42	Sequence 42, Appl
5	53	100.0	12	10 US-09-563-222-11	Sequence 11, Appl
6	53	100.0	12	12 US-10-379-741-8	Sequence 8, Appli
7	53	100.0	12	14 US-10-001-934-62	Sequence 62, Appl
8	53	100.0	12	15 US-10-374-932-8	Sequence 8, Appli
9	53	100.0	12	15 US-10-338-366-20	Sequence 20, Appl
10	53	100.0	12	15 US-10-275-046-19	Sequence 19, Appl
11	53	100.0	28	12 US-10-269-711-57	Sequence 57, Appl
12	53	100.0	74	14 US-10-125-687-23	Sequence 23, Appl
13	53	100.0	95	14 US-09-948-939-5	Sequence 5, Appli
14	53	100.0	95	14 US-10-041-860-371	Sequence 371, App
15	53	100.0	96	12 US-10-453-698-29	Sequence 29, Appl

16	53	100.0	96	14	US-10-194-375-82	Sequence 82, Appl
17	53	100.0	96	14	US-10-153-382-22	Sequence 22, Appl
18	53	100.0	96	14	US-10-041-860-10	Sequence 10, Appl
19	53	100.0	96	14	US-10-041-860-370	Sequence 370, App
20	53	100.0	96	14	US-10-041-860-376	Sequence 376, App
21	53	100.0	96	14	US-10-041-860-377	Sequence 377, App
22	53	100.0	96	15	US-10-308-817-29	Sequence 29, Appl
23	53	100.0	96	15	US-10-309-762-35	Sequence 35, Appl
24	53	100.0	101	14	US-10-010-729-31	Sequence 31, Appl
25	53	100.0	104	9	US-09-828-708-6	Sequence 6, Appli
26	53	100.0	105	9	US-09-828-708-3	Sequence 3, Appli
27	53	100.0	105	9	US-09-828-708-5	Sequence 5, Appli
28	53	100.0	105	9	US-09-828-708-7	Sequence 7, Appli
29	53	100.0	106	15	US-10-309-762-163	Sequence 163, App
30	53	100.0	107	15	US-10-309-762-38	Sequence 38, Appl
31	53	100.0	107	15	US-10-309-762-44	Sequence 44, Appl
32	53	100.0	107	15	US-10-309-762-80	Sequence 80, Appl
33	53	100.0	108	10	US-09-300-425B-21	Sequence 21, Appl
34	53	100.0	108	12	US-10-292-088-113	Sequence 113, App
35	53	100.0	108	12	US-10-269-711-21	Sequence 21, Appl
36	53	100.0	108	14	US-10-041-860-47	Sequence 47, Appl
37	53	100.0	108	14	US-10-041-860-49	Sequence 49, Appl
38	53	100.0	108	14	US-10-041-860-225	Sequence 225, App
39	53	100.0	108	14	US-10-041-860-226	Sequence 226, App
40	53	100.0	108	14	US-10-041-860-259	Sequence 259, App
41	53	100.0	108	14	US-10-041-860-260	Sequence 260, App
42	53	100.0	108	14	US-10-041-860-369	Sequence 369, App
43	53	100.0	108	14	US-10-041-860-375	Sequence 375, App
44	53	100.0	108	14	US-10-127-890-150	Sequence 150, App
45	53	100.0	108	14	US-10-321-558-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-828-708-38
; Sequence 38, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Burton, H.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-38

Query Match 100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12

Db 1 RASQSVSSSYLA 12

RESULT 2

US-09-828-708-40
; Sequence 40, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-40

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 3
US-09-828-708-41
; Sequence 41, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-41

Query Match
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 4
US-09-828-708-42
; Sequence 42, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-42

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RASQSVSSSYLA 12

RESULT 5
US-09-563-222-11
; Sequence 11, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-11

Query Match
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

RESULT 6
US-10-379-741-8
; Sequence 8, Application US/10379741
; Publication No. US20040071702A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Gerritsen, Arnout F.
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
; TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)
; FILE REFERENCE: GMI-024CE2
; CURRENT APPLICATION NUMBER: US/10/379,741
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/314,731
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-741-8

Query Match
Best Local Similarity 100.0%; Score 53; DB 12; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 1 RASQSVSSSYLA 12

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; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-338-366-20

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Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 RASQSVSSSYLA 12
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RESULT 10
US-10-275-046-19
; Sequence 19, Application US/10275046
; Publication No. US20040019187A1
; GENERAL INFORMATION:
; APPLICANT: Nagv et al.
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275,046
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: HLA-DR specific polypeptide
US-10-275-046-19

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RESULT 11
US-10-269-711-57
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; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; APPLICANT: Keeler, Tibor
; FILE REFERENCE: 6989.US.01
; CURRENT APPLICATION NUMBER: US/10/269,711

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; CURRENT FILING DATE: 2002-10-14
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-711-57

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US-10-125-687-23
; Sequence 23, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-687-23

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Db 17 RASQSVSSSYLA 28

US-09-948-939-5
; Sequence 5, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Haik, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 05/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain variable region predicted sequence for
US-09-948-939-5

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

US-10-041-860-371
; Sequence 371, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371
; LENGTH: 95
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 54
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: 54
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-371

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-453-698-29
; Sequence 29, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 96
; TYPE: PRT
; ORGANISM: human
US-10-453-698-29

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QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

US-10-041-860-371
; Sequence 371, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371
; LENGTH: 95
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 54
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: 54
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-371

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| | | | | | | | | |
Db 24 RASQVSSSYLA 35

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Job time : 36.1739 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 14.4348 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ4

Perfect score: 53

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Total number of hits satisfying chosen parameters: 389414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	53	100.0	108	1	US-08-488-113B-150
4	53	100.0	108	1	US-08-477-484B-150
5	53	100.0	108	2	US-08-646-360-150
6	53	100.0	108	2	US-08-232-081B-42
7	53	100.0	108	3	US-08-839-765-150
8	53	100.0	108	3	US-09-136-389-150
9	53	100.0	108	4	US-09-610-838-150
10	53	100.0	108	4	US-09-711-485-150
11	53	100.0	109	4	US-09-025-769B-16
12	53	100.0	110	4	US-09-025-769B-30
13	53	100.0	110	4	US-09-025-769B-47
14	53	100.0	116	1	US-08-053-131-183
15	53	100.0	116	2	US-08-096-762-183
16	53	100.0	116	3	US-09-042-353-46
17	53	100.0	116	4	US-08-758-417A-311
18	53	100.0	150	3	US-08-862-124-5
19	53	100.0	224	4	US-09-456-090A-40
20	53	100.0	224	4	US-09-456-090A-52
21	53	100.0	224	4	US-09-456-090A-76
22	53	100.0	226	4	US-09-456-090A-38
23	53	100.0	226	4	US-09-456-090A-42
24	53	100.0	226	4	US-09-456-090A-50
25	53	100.0	226	4	US-09-456-090A-80
26	53	100.0	226	4	US-09-456-090A-86
27	53	100.0	287	3	US-08-862-124-17

28	53	100.0	304	3	US-08-862-124-14	Sequence 14, Appl
29	52	98.1	108	3	US-09-240-274-178	Sequence 178, App
30	50	94.3	107	4	US-08-635-109-5	Sequence 5, Appl
31	50	94.3	109	1	US-08-278-852-147	Sequence 147, App
32	50	94.3	109	1	US-08-899-575-147	Sequence 147, App
33	50	94.3	109	1	US-08-899-575-147	Sequence 147, App
34	50	94.3	109	5	PCT-US95-08743-147	Sequence 147, App
35	50	94.3	224	4	US-09-456-090A-44	Sequence 44, Appl
36	50	94.3	224	4	US-09-456-090A-78	Sequence 78, Appl
37	49	92.5	112	1	US-08-276-852-151	Sequence 151, App
38	49	92.5	112	1	US-08-899-575-151	Sequence 151, App
39	49	92.5	112	1	US-08-899-575-151	Sequence 151, App
40	49	92.5	112	5	PCT-US95-08743-151	Sequence 151, App
41	49	92.5	226	4	US-09-456-090A-72	Sequence 72, Appl
42	49	92.5	226	4	US-09-456-090A-74	Sequence 74, Appl
43	48	90.6	129	2	US-08-480-774A-4	Sequence 4, Appl
44	48	90.6	141	4	US-09-472-087-88	Sequence 88, Appl
45	48	90.6	235	4	US-09-472-087-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-472-087-87
; Sequence 87, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-87

Query Match 100.0%; Score 53; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 24 RASQSVSSSYLA 35

RESULT 2
US-08-652-558-49
; Sequence 49, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA

;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/552,558
;; FILING DATE: JUNE 6, 1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/IB94/00387
;; FILING DATE: NOVEMBER 21, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YANKWICH, LEON R.
;; REGISTRATION NUMBER: 30,237
;; REFERENCE/DOCKET NUMBER: 95,497-L
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-345-9100
;; TELEFAX: 617-345-9111
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Protein
US-08-652-558-49

Query Match 100.0%; Score 53; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 24 RASQSVSSSYLA 35

RESULT 3
US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 108 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-488-113B-150

Query Match 100.0%; Score 53; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
DB 24 RASQSVSSSYLA 35

RESULT 4
US-08-477-484B-150
; Sequence 150, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 100.0%; Score 53; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 5
US-08-646-360-150
Sequence 150, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studzika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US/08/646.360
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-150

Query Match 100.0%; Score 53; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 6
US-08-232-081B-42
Sequence 42, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-42

Query Match 100.0%; Score 53; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

```
RESULT 7
US-08-839-765-150
; Sequence 150, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-150

Query Match 100.0%; Score 53; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 8
US-09-136-389-150
; Sequence 150, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-150

Query Match 100.0%; Score 53; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 9
US-09-610-838-150
; Sequence 150, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-389-150

Query Match 100.0%; Score 53; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35
```

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-150

Query Match 100.0%; Score 53; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 10
US-09-711-485-150
Sequence 150, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-150

Query Match 100.0%; Score 53; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 11
US-09-025-769B-16
Sequence 16, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 109 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-025-769B-16

Query Match 100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 12
US-09-025-769B-30
; Sequence 30, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0

;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 110 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-025-769B-30

Query Match 100.0%; Score 53; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
Db 24 RASQSVSSSYLA 35

RESULT 13
US-09-025-769B-47
; Sequence 47, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-47

Query Match 100.0%; Score 53; DB 4; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | |
Db 24 RASQSVSSSYLA 35

RESULT 14
US-08-053-131-183
; Sequence 183, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIORITY INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-131-183

Query Match 100.0%; Score 53; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | |
Db 44 RASQSVSSSYLA 55

RESULT 15
US-08-096-762-183
; Sequence 183, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils

; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-096-762-183

Query Match 100.0%; Score 53; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 12
| | | | | | | | | |
Db 44 RASQSVSSSYLA 55

Search completed: April 21, 2004, 17:40:04
Job time : 14.4348 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 3.55072 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: SEQ5

Perfect score: 31

Sequence: 1 atserat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	497	1 KPYC_ARATH	O65595 arabidopsis
2	28	90.3	5703	1 MUSB_HUMAN	Q9HC84 homo sapien
3	27	87.1	249	1 MARC_BOVIN	O02659 bos taurus
4	27	87.1	283	1 NI42_ARATH	Q8W036 arabidopsis
5	27	87.1	475	1 MMR_STRCO	P11545 streptomyce
6	27	87.1	676	1 VGP_EBOSB	Q66814 ebola virus
7	27	87.1	676	1 VGP_EBOSB	Q66798 ebola virus
8	27	87.1	695	1 PLB2_CANGA	Q8T906 candida gla
9	27	87.1	777	1 RTN1_RAT	Q64548 rattus norv
10	27	87.1	888	1 STU2_YEAST	P46675 saccharomyc
11	27	87.1	988	1 TERT_SCHPO	O13339 schizosacch
12	27	87.1	1153	1 NS2A_HUMAN	P35228 homo sapien
13	27	87.1	1464	1 NME1_MOUSE	P35436 mus musculu
14	27	87.1	1464	1 NME1_MOUSE	Q00959 rattus norv
15	26	83.9	268	1 RP30_HUMAN	P78346 homo sapien
16	26	83.9	367	1 TISD_MOUSE	P23949 mus musculu
17	26	83.9	429	1 CYSD_SCHPO	O13326 schizosacch
18	26	83.9	444	1 ARLY_SULSO	Q9UX32 sulfolobus
19	26	83.9	928	1 EZAL_ARATH	Q9Z8M8 arabidopsis
20	26	83.9	3255	1 MAY4_SCHCO	P37335 schizopyll
21	26	83.9	3255	1 POLG_LMVO	P31999 l genome po
22	26	83.9	3255	1 POLG_LMVE	P89876 l genome po
23	25	80.6	94	1 RL43_SCHPO	O94686 schizosacch
24	25	80.6	156	1 PHS_FAGGE	O52077 fagus crena
25	25	80.6	182	1 PACA_CLANA	P48144 clarias mac
26	25	80.6	195	1 XINA_BACST	P45705 bacillus st
27	25	80.6	210	1 Y215_ADE02	P05038 mus musculu
28	25	80.6	215	1 Y215_ADE02	Q01622 helobdella
29	25	80.6	429	1 MAD_MOUSE	P40688 drosophila
30	25	80.6	548	1 SNA_DROME	P22757 paracentrot
31	25	80.6	587	1 HE_FRLI	O33137 mycobacteri
32	25	80.6	587	1 REC_N_MYCTU	
33	25	80.6	587	1 REC_N_MYCTU	

ALIGNMENTS

RESULT 1

KPYC_ARATH STANDARD; PRT; 497 AA.

ID KPYC_ARATH STANDARD; PRT; 497 AA.

AC O65595;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Probable pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK).

GN A14G36390 OR M3E9.180

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

ON NCBI_TaxID=3702;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083486; PubMed=10617198;

RA Mayer K.F.X., Schueeller C., Wambutt R., Murphy G., Volckaert G.,

RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,

RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,

RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,

RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dircke W.,

RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

RA De Keyser A., Buysshaert C., Gielens J., Villarroel R., De Clercq R.,

RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,

RA Pettett A., Rajadream M.A., Lyne M., Benes V., Rechmann S.,

RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,

RA Dose S., de Raan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fartmann B., Granderath K., Bauner D., Herzl A.,

RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,

RA Massenat O., Quigley F., Claubald G., Muendlein A., Felber R.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

RA Cheford F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,

RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,

RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,

RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang B., Spiegel L.,

RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

RA Stoneking T., Kalicki J., Graves T., Haymon G., Edwards J.,

RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,

RA Kramers J., Fulton L., Mardis E., Dance M., Pepin K., Hillier L.W.,

RA Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,

RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,

34 25 80.6 1018 1 YDIJ_ECOLI
35 25 80.6 1027 1 YDIJ_ECOLI
36 24 77.4 119 1 YPAA_LACLA
37 24 77.4 180 1 PSP2_CABEL
38 24 77.4 202 1 COAT_ELV
39 24 77.4 229 1 YTE7_CABEL
40 24 77.4 265 1 HMEC_XENLA
41 24 77.4 325 1 YHU3_YEAST
42 24 77.4 328 1 SGS3_DROER
43 24 77.4 337 1 CAHE_MOUSE
44 24 77.4 361 1 COL9_ARATH
45 24 77.4 374 1 RECA_STRCO

P77748 escherichia
Q57252 haemophilus
Q02009 lactococcus
O62193 caenorhabdi
P35927 erysimum la
Q11083 caenorhabdi
P52729 xenopus lae
P38844 saccharomyc
P13730 drosophila
Q9WV66 mus musculu
O22800 arabidopsids
O50487 streptomyce

RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Gracat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
RN
CC -1- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
CC -1- COFACTOR: Requires magnesium and potassium.
CC -1- PATHWAY: Glycolysis; final step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the pyruvate kinase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC ENBL; AL022223; CAA18231.1; -;
CC ENBL; AL161565; CAB79494.1; -;
CC PIR; T05065; T05065.
CC HSP; P14178; I80T.
CC InterPro; IPR001697; Pyruvate_kinase.
CC Pfam; PF02287; PK_C1.
CC PRINTS; PR01050; PYRUV_KINASE.
CC PRODOM; PD001009; Pyruvate_kinase; 1.
CC TRIFAMS; TIGR01064; PYRUV_KIN; 1.
CC PROSITE; PS00110; PYRUVATE_KINASE; 1.
CC Transferase; Kinase; Glycolysis; Magnesium.
KW ACT_SITE 227 227 BY SIMILARITY.
FT METAL 229 229 MAGNESIUM (BY SIMILARITY).
FT METAL 250 250 MAGNESIUM (BY SIMILARITY).
FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 497 AA; 54319 MW; 45D43EF54A99F662 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATSSRAT 7
Db 377 ATSSRAT 383
RESULT 2
ID MUC5B HUMAN STANDARD; PRT; 5703 AA.
AC Q9HC64; Q00447; Q00573; Q14985; Q15494; Q95291; Q95451; Q14881;
AC Q9552; Q9UE28;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mucin 5B precursor (Mucin 5 subtype B, tracheobronchial) (High
DE molecular weight salivary mucin MGI) (Sublingual gland mucin).
GN MUC5B OR MUC5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-1594 FROM N.A.
RA Chen Y., Di Y.P., Wu R.;
RT "Molecular cloning of the amino-terminal and 5'-flanking region of the
RT human MUC5B mucin gene.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-1325 FROM N.A.

RX MEDLINE=99009274; PubMed=9790959;
RA Offner G.D., Nunes D.P., Keates A.C., Afdhal N.H., Troxler R.P.;
RT "The amino-terminal sequence of MUC5B contains conserved
RT multifunctional D domains: implications for tissue-specific mucin
RT functions.";
RL Biochem. Biophys. Res. Commun. 251:350-355(1998).
RN [3]
RP SEQUENCE OF 40-1324 FROM N.A.
RX MEDLINE=99029332; PubMed=9804771;
RA Desseyn J.-L., Buisine M.P., Porchet N., Aubert J.-P., Laine A.;
RT "Genomic organization of the human mucin gene MUC5B: cDNA and genomic
RT sequences upstream of the large central exon.";
RL J. Biol. Chem. 273:30157-30164(1998).
RN [4]
RP SEQUENCE OF 1326-4895 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97166151; PubMed=9013550;
RA Desseyn J.-L., Guyonnet-Duperat V., Porchet N., Aubert J.-P.,
RA Laine A.;
RT "Human mucin gene MUC5B, the 10.7 kb large central exon encodes
RT various alternate subdomains resulting in a super-repeat. Structural
RT evidence for a 11p15.5 gene family.";
RL J. Biol. Chem. 272:3168-3178(1997).
RN [5]
RP SEQUENCE OF 4057-4480 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=97292540; PubMed=9147051;
RA Nielsen P.A., Bennett E.P., Wandall H.H., Therkildsen M.H.,
RA Hannibal J., Clausen H.;
RT "Identification of a major human high molecular weight salivary mucin
RT (MGI) as tracheobronchial mucin MUC5B.";
RL Glycobiology 7:413-419(1997).
RN [6]
RP SEQUENCE OF 4721-5703 FROM N.A.
RC TISSUE=Gall bladder;
RX MEDLINE=97293229; PubMed=9164870;
RA Keates A.C., Nunes D.P., Afdhal N.H., Troxler R.P., Offner G.D.;
RT "Molecular cloning of a major human gall bladder mucin: complete C-
RT terminal sequence and genomic organization of MUC5B.";
RL Biochem. J. 324:295-303(1997).
RN [7]
RP SEQUENCE OF 4809-5687 FROM N.A.
RC TISSUE=Sublingual gland;
RX MEDLINE=96125355; PubMed=8554565;
RA Troxler R.P., Offner G.D., Zhang F., Iontcheva I., Oppenheim F.G.;
RT "Molecular cloning of a novel high molecular weight mucin (MGI)
RT from human sublingual gland.";
RL Biochem. Biophys. Res. Commun. 217:1112-1119(1995).
RN [8]
RP SEQUENCE OF 4859-5703 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97347489; PubMed=9201995;
RA Desseyn J.-L., Aubert J.-P., Porchet N., Laine A.;
RT "Genomic organization of the 3 region of the human MUC5B mucin.";
RL J. Biol. Chem. 272:16873-16883(1997).
CC -1- FUNCTION: Salivary mucin that is thought to contribute to the
CC lubricating and viscoelastic properties of whole saliva.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- TISSUE SPECIFICITY: Expressed mainly in bronchus glands and also
CC in submaxillary glands, endocervix, gall bladder, and pancreas.
CC -1- PTM: Highly glycosylated.
CC -1- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
CC -1- SIMILARITY: Contains 3 VWFC domains.
CC -1- SIMILARITY: Contains 4 VWFD domains.
CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
CC
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CC or send an email to license@isb-sib.ch).

RC STRAIN=A3(2);
RX MEDLINE=88112873; PubMed=2828187;
RA Neal R.J., Chater K.F.;
RT "Nucleotide sequence analysis reveals similarities between proteins
RT determining methylenomycin A resistance in Streptomyces and
RT tetracycline resistance in eubacteria";
RL Gene 58:229-241(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bruton C.J., Wietzorrek A., Hartley N., Woodburn L., Chater K.F.;
RT "Genes involved in methylenomycin biosynthesis from plasmid SCP1 of
RT Streptomyces coelicolor A3(2)";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Huang C., Fraser A., Goble L., Hidaigo J., Hornsby T., Howarth S.,
RA Cronin A.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: RESISTANCE TO THE EPOXIDE ANTIBIOTIC METHYLENOMYCIN A;
CC PROBABLY BY MEDIATING ITS EFFLUX.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M18263; AAA98341.1; -;
DR EMBL; AJ276673; CAB82871.1; -;
DR EMBL; AL589148; CAC32711.1; -;
DR EMBL; AL590464; CAC36763.1; -;
DR F01; B29606; B29606.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS0850; MFS; 1.
KW Plasmid; Antibiotic resistance; Transmembrane; Transport;
KW Complete proteome.
FT TRANSMEM 28 48 POTENTIAL.
FT TRANSMEM 65 85 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 173 193 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 285 305 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 346 366 POTENTIAL.
FT TRANSMEM 371 391 POTENTIAL.
FT TRANSMEM 416 436 POTENTIAL.
FT TRANSMEM 439 459 POTENTIAL.
SQ SEQUENCE 475 AA; 49238 MW; CF35F49BA9535102 CRC64;
Query Match 87.1%; Score 27; DB 1; Length 475;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATSSRAT 7
Db 204 ATESRAT 210
RESULT 6
VGP_EBOSB
ID VGP_EBOSB STANDARD; PRT; 676 AA.
AC Q66814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Structural glycoprotein precursor (Viron spike glycoprotein)
DE [Contains: GP1; GP2].
GN GP.
OS Ebola virus (strain Sudan Boniface) (Ebo).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Ebola-like viruses.
OX NCBI_TaxID=128948;
RN [1]
RP SEQUENCE FROM N.A. AND RNA EDITING.
RX MEDLINE=96195018; PubMed=8622982;
RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
RT "The virion glycoproteins of Ebola viruses are encoded in two reading
RT frames and are expressed through transcriptional editing";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
CC -!- FUNCTION: Structural protein that forms the virion spike and which
CC is responsible for binding to target cells and subsequent fusion
CC of the viral and host-cell membranes. In cell receptor recognition
CC and in fusion.
CC -!- SUBUNIT: Homotrimer; each monomer consist of a GP1 and a GP2
CC subunit linked by disulfide bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. GP1 can also be
CC shed by the virus after proteolytic processing (By similarity).
CC -!- PTM: N-glycosylated, could also be O-glycosylated (By similarity).
CC -!- PTM: Processing into GP1 and GP2 is effected by the host furin (By
CC similarity).
CC -!- RNA EDITING: Modified positions=295; Note=Partially edited. RNA
CC editing at this position consists of an insertion of one adenine
CC nucleotide. The sequence displayed here is the full-length
CC transmembrane glycoprotein, derived from the edited RNA. The
CC unedited RNA gives rise to the small secreted glycoprotein (AC
CC P60172).
CC -!- SIMILARITY: Belongs to the filoviruses glycoprotein family.
CC -----
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CC -----
CC EMBL; U28134; AAB37096.1; -;
DR HSP; Q05320; 2EBO.
DR InterPro; IPR002561; Filo_glycop.
DR Pfam; PF01611; Filo_glycop; 1.
KW Transmembrane; Envelope protein; Glycoprotein; Signal; RNA editing.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 676 STRUCTURAL GLYCOPROTEIN.
FT CHAIN 33 501 GP1.
FT CHAIN 502 676 GP2.
FT DOMAIN 33 649 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 650 672 POTENTIAL.
FT DOMAIN 673 676 CYTOPLASMIC (POTENTIAL).
FT DISULFID 601 608 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 676 AA; 74986 MW; 700029BFD67F5E9A CRC64;

Query Match 87.1%; Score 27; DB 1; Length 676;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRT 7
Db 321 ATSSRT 327

RESULT 7
VGP_EBOSM
ID - VGP_EBOSM STANDARD; PRT; 676 AA.
AC Q66798;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Structural glycoprotein precursor (Virion spike glycoprotein)
DE [Contains: GP1; GP2].
GN GP.
OS Ebola virus (strain Sudan Maleo-79) (Ebo).
OC Viruses; sRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Ebola-like viruses.
OX NCBI_TaxID=128949;
RN [1]
SEQUENCE FROM N.A., AND RNA EDITING.
RX MEDLINE=96195018; PubMed=8622982;
RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
RT "The virion glycoproteins of Ebola viruses are encoded in two reading
frames and are expressed through transcriptional editing.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
CC -!- FUNCTION: Structural protein that forms the virion spike and which
is responsible for binding to target cells and subsequent fusion
of the viral and host-cell membranes. In cell receptor recognition
and in fusion.
CC -!- SUBUNIT: Homotrimer; each monomer consist of a GP1 and a GP2
subunit linked by disulfide bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. GP1 can also be
shed by the virus after proteolytic processing (By similarity).
CC -!- PTM: N-glycosylated, could also be O-glycosylated (By similarity).
CC -!- PTM: Processing into GP1 and GP2 is effected by the host furin (By
similarity).
CC -!- RNA EDITING: Modified positions=295; Note-Partially edited. RNA
editing at this position consists of an insertion of one adenine
nucleotide. The sequence displayed here is the full-length
transmembrane glycoprotein, derived from the edited RNA. The
unedited RNA gives rise to the small secreted glycoprotein (AC
P60173).
CC -!- SIMILARITY: Belongs to the filoviruses glycoprotein family.

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EMBL; U23069; AAC54882.1; -.
DR HSPG; Q05320; ZEB0.
DR InterPro; IPR002561; Filo_glycop.
DR Pfam; PF01611; Envloprote; 1.
KW Transmembrane; Filovirus protein; Glycoprotein; Signal; RNA editing.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 676 STRUCTURAL GLYCOPROTEIN.
FT CHAIN 33 501 GP1.
FT CHAIN 502 676 GP2.

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FT DOMAIN 33 649 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 650 672 POTENTIAL.
FT DOMAIN 673 676 CYTOPLASMIC (POTENTIAL).
FT DISULFID 601 608 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 676 AA; 74970 MW; 1DAB9EB78CF755C8 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 676;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRT 7
Db 321 ATSSRT 327

RESULT 8
PLB2_CANGA
ID - PLB2_CANGA STANDARD; PRT; 695 AA.
AC Q8TG06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lysophospholipase 2 precursor (EC 3.1.1.5) (Phospholipase B 2).
GN PLB2.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
SEQUENCE FROM N.A.
RA Clancy C., Cheng S., Chekley M.A., Lewin A., Nguyen M.-H.;
RT "Cloning and characterization of phospholipase B gene (PLB2) of Candida
glabrata".
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the release of fatty acids from
lysophospholipids. Phospholipase B may well contribute to
pathogenicity by abetting the fungus in damaging and traversing
host cell membranes, processes which likely increase the rapidity
of disseminated infection (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
glycerophosphocholine + a fatty acid anion.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the lysophospholipase family.

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EMBL; AF498582; AAM19335.1; -.
DR InterPro; IPR02642; PLAC.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00022; PLAC; 1.
KW Lipid degradation; Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 695 LYSPHOSPHOLIPASE 2.
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

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CC -!- FUNCTION: May play a role in the attachment, organization, and/or
CC dynamics of microtubule ends at the spindle pole body.
CC -!- SUBUNIT: Binds to microtubules.
CC -!- SUBCELLULAR LOCATION: LOCALIZES PRIMARILY TO THE SPINDLE POLE BODY
CC (SPB) AND TO A LESSER EXTENT ALONG SPINDLE MICROTUBULES.
CC -!- MISCELLANEOUS: Mutations in STU2 suppress a cold-sensitive
CC mutation in TUB2.
CC -!- SIMILARITY: Belongs to the TOG/XMAP215 family.
CC -!- SIMILARITY: Contains 2 HEAT repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U35247; AAA79057.1; -
CC EMBL; X94607; CAA64292.1; -
CC EMBL; Z73217; CAA97574.1; -
CC PIR; S61619; S61619.
CC GerMOnline; 142107; -.
CC SGD; S0004035; STU2.
CC GO; GO:0005816; C:spindle pole body; IDA.
CC GO; GO:0008017; F:microtubule binding; IMP.
CC GO; GO:0005200; F:structural constituent of cytoskeleton; IPI.
CC GO; GO:0007020; P:mitotubule nucleation; IPI.
CC GO; GO:0000071; P:mitotic spindle assembly (sensu Saccharomycetes); IGI.
CC InterPro; IPR008938; ARM.
CC InterPro; IPR000357; HEAT.
CC PROSITE; PS50077; HEAT_REPEAT; 1.
CC Repeat; Microtubule.
CC REPEAT 453 490 HEAT 1.
CC REPEAT 498 535 HEAT 2.
CC FT REPEAT 498 535
CC SQ SEQUENCE 888 AA; 100918 MW; 7A49C3702E21C7BF CRC64;

Query Match 87.1%; Score 27; DB 1; Length 888;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
DB 113 TSSRAT 118

RESULT 11
ID TERT SCHPO STANDARD; PRT; 988 AA.
AC 013339; 013338;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit).
GN TERT OR SPBC29A3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,
RA Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human.";
RL Science 277:955-959 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leach S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Wellens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel K., Fuchs M., Fritsch C., Holzer H., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinhardt R., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.D., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC single sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O13339-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O13339-2; Sequence=VSP_006395;
CC -!- MISCELLANEOUS: DELETION CAUSES TELOMERASE SHORTENING AND SENESENCE.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -----
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CC -----
CC EMBL; AF015783; AAC49802.1; -
CC EMBL; AF015783; AAC49803.1; -
CC EMBL; AL022299; CAA18391.1; -
CC PIR; T03838; T03838.
CC GeneDB SPombe; SPBC29A3.14C; -.
CC InterPro; IPR000477; RVTse.
CC InterPro; IPR003545; Telomerase_RT.
CC Pfam; PF00078; rvt; 2.
CC PRINTS; PR01365; TELOMERASERT.
CC Transferrase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
CC DNA-binding; Alternative splicing.
CC FT VARSPPLIC 524 524 K -> KQ (in isoform 2).
CC FT SEQUENCE 988 AA; 116328 MW; AB2DC7030228F443 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 988;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 626 ATSDRAT 632

```

RESULT 12
ID NS2A HUMAN STANDARD; PRT; 1153 AA.
AC P35228; O60757; O94994; Q16263; Q16692;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Hepatocyte NOS) (HEP-NOS).
GN NOS2A OR NOS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93234523; PubMed=7682706;
RA Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,
RA di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,
RA Billiar T.R.;
RT "Molecular cloning and expression of inducible nitric oxide synthase
RT from human hepatocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colorectal adenocarcinoma;
RX MEDLINE=94032282; PubMed=7692964;
RA Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;
RT "Purification and cDNA sequence of an inducible nitric oxide synthase
RT from a human tumor cell line.";
RL Biochemistry 32:11600-11605 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Chondrocytes;
RX MEDLINE=94068614; PubMed=7504305;
RA Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,
RA Chubb A.P., Hall V.S., Moss D.W., Moncada S.;
RT "Cloning, characterization, and expression of a cDNA encoding an
RT inducible nitric oxide synthase from the human chondrocyte.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423 (1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular chondrocytes;
RX MEDLINE=94368816; PubMed=7522054;
RA Maier R., Bilbe G., Rediske J., Lotz M.;
RT "Inducible nitric oxide synthase from human articular chondrocytes:
RT cDNA cloning and analysis of mRNA expression.";
RL Biochim. Biophys. Acta 1208:145-150 (1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=95091827; PubMed=7528017;
RA Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;
RT "Human retina expresses both constitutive and inducible isoforms of
RT nitric oxide synthase mRNA.";
RL Biochem. Biophys. Res. Commun. 205:85-91 (1994).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Glioblastoma;
RX MEDLINE=95155267; PubMed=7531687;
RA Hokari A., Zeniya M., Saumi H.;
RT "Cloning and functional expression of human inducible nitric oxide
RT synthase (NOS) cDNA from a glioblastoma cell line A-172.";
RL J. Biochem. 116:575-581 (1994).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Airway epithelium;
RX MEDLINE=95372368; PubMed=7544004;
RA Guo F.H., de Raave R.H., Rice T.W., Stuehr D.J., Thummesen F.B.J.M.,
RA Erzurum S.C.;
RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase
RT in normal human airway epithelium in vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813 (1995).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiac myocytes;
RX MEDLINE=97304504; PubMed=9160867;
RA Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T.,
RA Hatakeyama K., Geller D.A., Mickie D.A.G., Simmons R.L.,
RA Billiar T.R.;
RT "Differentiated human ventricular cardiac myocytes express
RT inducible nitric oxide synthase mRNA but not protein in response to
RT IL-1, TNF, IFN-gamma, and LPS.";
RL J. Mol. Cell. Cardiol. 29:1153-1165 (1997).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney;
RX MEDLINE=95165725; PubMed=7532448;
RA McLeay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,
RA Ralston S.H., Grabowski P., Hailes N.E., Macleod A.M.,
RA Hawksworth G.M.;
RT "Nitric oxide production by human proximal tubular cells: a novel
RT immunomodulatory mechanism.";
RL Kidney Int. 46:1043-1049 (1994).
RN [11]
RP CHARACTERIZATION.
RX MEDLINE=96047340; PubMed=7558036;
RA Bloch K.D., Wolfgram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,
RA Lepore J.J., Philippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
RT "Three members of the nitric oxide synthase II gene family (NOS2A,
RT NOS2B, and NOS2C) colocalize to human chromosome 17.";
RL Genomics 27:526-530 (1995).
RN [12]
RP CHARACTERIZATION.
RX MEDLINE=98398965; PubMed=9721329;
RA Taylor B.S., Alarcon L.H., Billiar T.R.;
RT "Inducible nitric oxide synthase in the liver: regulation and
RT function.";
RL Biochimica 63:766-781 (1998).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.
RX MEDLINE=99340057; PubMed=10409685;
RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,
RA Whitlow M., Poulos T.L.;
RT "Crystal structures of zinc-free and -bound heme domain of human
RT inducible nitric-oxide synthase. Implications for dimer stability and
RT comparison with endothelial nitric-oxide synthase.";
RL J. Biol. Chem. 274:21276-21284 (1999).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.
RX MEDLINE=99173237; PubMed=10074942;
RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
RA Dolphin B., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
RA Weber P.C.;
RT "Structural characterization of nitric oxide synthase isoforms
RT reveals striking active-site conservation.";
RL Nat. Struct. Biol. 6:233-242 (1999).
CC -I- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
CC with diverse functions throughout the body. In macrophages, NO
CC mediates tumoricidal and bactericidal actions.
CC -I- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -I- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme (by similarity).
CC -I- ENZYME REGULATION: Regulated by calcium/calmodulin (in contrast
CC with mouse NOS2). Aspirin inhibits expression and function of this
CC enzyme and effects may be exerted at the level of

translational/posttranslational modification and directly on the catalytic activity (By similarity).

-1- SUBUNIT: Homodimer.

-1- ALTERNATIVE PRODUCTS:

Event-alternative splicing; Named isoforms=2;

Name=1;

isoId=P35228-1; Sequence=Displayed;

Name=2;

isoId=P35228-2; Sequence=VSP_003583;

TISSUE SPECIFICITY: Expressed in the liver, retina, bone cells and airway epithelial cells of the lung. Not expressed in the placenta.

-1- INDUCTION: By endotoxins and cytokines.

-1- SIMILARITY: Belongs to the NOS family.

-1- SIMILARITY: Contains 1 flavodoxin-like domain.

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EMBL; L09210; AAA59171.1; -

EMBL; L24553; AAA36375.1; -

EMBL; X73029; CAA51512.1; -

EMBL; U05810; AAA56666.1; -

EMBL; U31511; AAB34904.1; -

EMBL; D26525; BAA05531.1; -

EMBL; U20141; AAB60366.1; -

EMBL; AF068236; AAC19133.1; -

EMBL; AB022318; BAA37123.1; -

EMBL; S75615; AAD14179.1; -

PIR; A49676; A49676.

PDB; 1NSI; 07-JAN-00.

PDB; 2NSI; 07-JAN-00.

PDB; 4NOS; 04-FEB-00.

Genew; HGNC:7873; NOS2A.

MM; 163730; -

GO; GO:0005737; C.cytosolasm; TAS.

GO; GO:0004517; F.nitric-oxide synthase activity; TAS.

InterPro; IPR003097; FAD_Binding.

InterPro; IPR008254; Flav_nitox_synth.

InterPro; IPR001094; Flavodoxin-like.

InterPro; IPR001709; FPN_cyt_redctse.

InterPro; IPR004030; NO_synthase.

InterPro; IPR001433; OxRed_FAD/NAD(P).

Pfam; PF00567; FAD_binding_1; 1.

Pfam; PF00258; flavodoxin; 1.

Pfam; PF00175; NAD_binding_1; 1.

Pfam; PF02898; NO_synthase; 1.

PRINTS; PR00369; FLAVODOXIN.

PRINTS; PR00371; FPNCR.

PROSITE; PS50902; FLAVODOXIN-LIKE; 1.

PROSITE; PS50001; NOS; 1.

Oxidoreductase; NADP; FAD; FPN; Calcium-binding; Calmodulin-binding;

Query Match 87.1%; Score 27; DB 1; Length 1153;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7

Db 747 TSSRAT 752

RESULT 13

NME1_MOUSE

ID NME1_MOUSE STANDARD; PRT; 1464 AA.

AC P35436; 1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Glutamate [NMDA] receptor subunit epsilon 1 precursor (N-methyl D-aspartate receptor subtype 2A) (NR2A) (NMDAR2A).

GRIN2A.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

MEDLINE=92244361; PubMed=1374164;

Meguro H., Mori H., Araki K., Kushiya E., Kutsuwada T., Yamazaki M., Kumanishi T., Arakawa M., Sakimura K., Mishina M.; "Functional characterization of a heteromeric NMDA receptor channel expressed from cloned cDNAs."; Nature 357:70-74 (1992).

-1- FUNCTION: NMDA receptor subtype of glutamate-gated ion channels possesses high calcium permeability and voltage-dependent sensitivity to magnesium and is mediated by glycine.

-1- SUBUNIT: Heterodimer of an epsilon subunit and a zeta subunit. Interacts with AIP1 (By similarity).

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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EMBL; D10217; BAA01069.1; -

PIR; S29159; S29159.

HSSP; P19491; IGR2.

MED; MGI:195820; Grin2a.

GO; GO:0045211; C.postsynaptic membrane; IDA.

InterPro; IPR001320; Ion_glu_receptor.

InterPro; IPR001508; NMDA_receptor.

InterPro; IPR001311; SBP_glu_receptor.

Pfam; PF00060; lig_chan; 1.

PRINTS; PR00177; NMDARECEPTOR.

SMART; SM00079; PBPe; 1.

Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Calcium; Magnesium.

SIGNAL 1 22

CHAIN 23 1464

DOMAIN 23 555

TRANSMEM 556 576

TRANSMEM 593 613

TRANSMEM 634 654

TRANSMEM 817 837

TRANSMEM 614 614

SITE 75

CARBOHYD 340 340

CARBOHYD 380 380

CARBOHYD 443 443

CARBOHYD 444 444

CARBOHYD 541 541

SEQUENCE 1464 AA; 165490 MW; 422CD68C56379047 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 1464;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7

Db 1064 TSSRAT 1069

RESULT 14


```

CC  -!- SIMILARITY: BELONGS TO THE RPE1/RNASEP2 FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U77665; AAC51143.1; -.
DR  EMBL; AL590622; CAC70100.1; -.
DR  EMBL; BC006991; AAH06991.1; -.
DR  GK; F78346; -.
DR  MIM; 606115; -.
DR  GO; GO:0005655; C:nucleolar ribonuclease P complex; TAS.
DR  GO; GO:0005634; C:nucleus; TAS.
DR  GO; GO:0004526; F:ribonuclease P activity; TAS.
DR  InterPro; IPR002738; RNase_P_p30.
DR  Pfam; PF01876; RNase_P_D30; 1
KW  Hydrolase; Nuclear protein; tRNA processing; Antigen.
FT  CONFLICT 189 189 S -> I (IN REF. 1; AA SEQUENCE).
SQ  SEQUENCE 268 AA; 29321 MW; 2AB492D9BACDCBB CRC64;

Query Match      83.9%; Score 26; DB 1; Length 268;
Best Local Similarity 100.0%; Pred.No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ATSSRA 6
DB  92 ATSSRA 97

```

Search completed: April 21, 2004, 17:34:01
Job time : 5.55072 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 6.3913 seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ5

Perfect score: 31

Sequence: 1 atssrat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	31	100.0	497	2	T05065	pyruvate kinase (E
2	28	90.3	91	2	S37511	Ig kappa chain V r
3	28	90.3	482	2	S77660	ribosomal protein
4	28	90.3	543	2	S35047	mucin JUL7 - human
5	28	90.3	3570	2	T45025	mucin MUC5B, trach
6	27	87.1	93	2	S37501	Ig kappa chain V r
7	27	87.1	124	2	S20633	Ig kappa chain - h
8	27	87.1	131	2	E72469	hypothetical prote
9	27	87.1	227	2	B37473	envelope antigen h
10	27	87.1	228	2	T47425	NAC domain-like pr
11	27	87.1	410	2	B55223	aromatic dioxygena
12	27	87.1	475	2	B29606	methylmenocin A r
13	27	87.1	490	2	T04004	probable cytochrom
14	27	87.1	511	2	AG3470	glycerol-3-phospha
15	27	87.1	622	2	AG0001	potassium transpor
16	27	87.1	888	2	S61619	Str2 protein - yea
17	27	87.1	989	2	T03838	telomerase catalyt
18	27	87.1	1153	2	A49676	nitric-oxide synth
19	27	87.1	1464	1	S29159	glutamate receptor
20	27	87.1	1464	2	A43274	N-methyl D-asparta
21	26	83.9	51	2	E82855	hypothetical prote
22	26	83.9	128	2	S20636	Ig kappa chain V r
23	26	83.9	167	2	A72626	hypothetical prote
24	26	83.9	214	2	A46629	mucin 6, gastric (
25	26	83.9	280	2	T48434	hypothetical prote
26	26	83.9	314	2	A13041	ornithine cyclodea
27	26	83.9	328	2	C98244	ornithine cyclodea
28	26	83.9	346	2	T51377	hypothetical prote
29	26	83.9	355	1	G69309	conserved hypothet

30	26	83.9	367	2	C39590	TPA-induced protei
31	26	83.9	429	2	T40463	O-acetylhomoserine
32	26	83.9	433	2	S31436	Ig upsilon chain -
33	26	83.9	459	2	D90211	argininosuccinate
34	26	83.9	504	2	S75310	gumB protein . Syn
35	26	83.9	507	2	G70649	probable DNA ligas
36	26	83.9	719	2	T33170	hypothetical prote
37	26	83.9	750	2	T04980	hypothetical prote
38	26	83.9	856	2	T52415	polycarb protein E
39	26	83.9	898	2	T01503	hypothetical prote
40	26	83.9	928	2	C37271	A-alpha Y 4 protei
41	26	83.9	928	2	T16759	hypothetical prote
42	26	83.9	1966	2	T32552	hypothetical prote
43	26	83.9	2848	2	T32550	hypothetical prote
44	25	80.6	94	2	T40691	ribosomal protein
45	25	80.6	126	2	H72486	hypothetical prote

ALIGNMENTS

RESULT 1

T05065
Pyruvate kinase (EC 2.7.1.40) - Arabidopsis thaliana

N;Alternate names: protein M3E9.180

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999

C;Accession: T05065

R;Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hoheisel, J.; Mewes, H.W.; Mayer,

submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15396

A;Accession: T05065

A;Molecule type: DNA

A;Residues: 1-497 <BEV>

A;Cross-references: EMBL:AL022223

A;Experimental source: cultivar Columbia; BAC clone M3E9

C;Genetics:

A;Map position: 4

A;Introns: 73/3; 227/3

A;Note: M3E9.180

C;Superfamily: pyruvate kinase

C;Keywords: glycolysis; phosphotransferase

Query Match 100.0%; Score 31; DB 2; Length 497;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7

Db 377 ATSSRAT 383

RESULT 2

S37511
Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37511

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood.

A;Reference number: S37501

A;Accession: S37511

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-91 <KLE>

A;Cross-references: EMBL:Z26600; NID:g405664; PIDN:CAA81354.1; PID:g405665

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match 90.3%; Score 28; DB 2; Length 91;

Best Local Similarity 85.7%; Pred. No. 9;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: EMBL:Z72496; NID:G1834502; PIDN:CAA96577.1; PID:G1834503
A;Experimental source: placenta
C;Genetics:
A;Gene: MUC5B

Query Match      90.3%; Score 28; DB 2; Length 3570;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 1681 ATSSKAT 1687

RESULT 6
S37501
IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R;Klein, U.; Kueppers, R.; Rajewsky, K.
A;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37501
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <KLE>
A;Cross-references: EMBL:Z26611; NID:G405643; PIDN:CAA81364.1; PID:G405644
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match      87.1%; Score 27; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TSSRAT 7
Db 35 TSSRAT 40

RESULT 7
S20633
IG kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Accession: S20633
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
A;Description: Human IGM(+) IGD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S20633
A;Accession: S20633
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-124 <LEP>
A;Cross-references: EMBL:Z11891; NID:G33185; PIDN:CAA77945.1; PID:G33186
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;32-107/Domain: immunoglobulin homology <IMW>

Query Match      87.1%; Score 27; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TSSRAT 7
Db 68 TSSRAT 73

RESULT 8

```

```

E72469
hypothetical protein APE2398 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E72469
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72469
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-131 <KAW>
A:CROSS-references: DBJ:AP000064; NID:G5105945; PIDN:BAAB1413.1; PID:dl045199; PID:G510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2398

Query Match      87.1%; Score 27; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      38 TSSRAT 43

RESULT 9
B37473
envelope antigen homolog F3R - Orf virus
C:Species: Orf virus
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: B37473
R:Fleming, S.B.; Blok, J.; Fraser, K.M.; Mercer, A.A.; Robinson, A.J.
Virology 195, 175-184, 1993
A:Title: Conservation of gene structure and arrangement between vaccinia virus and orf v
A:Reference number: A37473; MUID:93303916; PMID:8317094
A:Accession: B37473
A>Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-227 <FLE>
A:CROSS-references: GB:S62819; NID:G386384; PIDN:AAB27258.1; PID:G386386
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:134136, NCBIF:134138)
A:Note: strain N22
C:Superfamily: vaccinia virus H6 protein

Query Match      87.1%; Score 27; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      118 TSSRAT 123

RESULT 10
T47425
NAC domain-like protein - Arabidopsis thaliana
N:Alternate names: protein T22K7.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47425
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T47425
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-228 <RIE>
A:CROSS-references: EMBL:ALJ38641
A:Experimental source: cultivar Columbia; BAC clone T22K7

```

```

C:Genetics:
A:Map position: 3
A:Introns: 53/1; 147/3
A:Note: T22K7.30

Query Match      87.1%; Score 27; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      175 TSSRAT 180

RESULT 11
B55523
aromatic dioxygenase (EC 1.14.-.-) ferredoxin reductase component - Pseudomonas sp. (stri
C:Species: Pseudomonas sp.
C>Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 20-Jun-2000
C:Accession: B55523
R:Kikuchi, Y.; Nagata, Y.; Hinata, M.; Kimbara, K.; Fukuda, M.; Yano, K.; Takagi, M.
J. Bacteriol. 176, 1689-1694, 1994
A:Title: Identification of the bphA4 gene encoding ferredoxin reductase involved in biph
A:Reference number: A55523; MUID:94179104; PMID:8132464
A:Accession: B55523
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-410 <KIK>
A:CROSS-references: GB:D16831; NID:G391830; PIDN:BAAB04112.1; PID:G431770
C:Superfamily: toluene dioxygenase ferredoxin reductase component
C:Keywords: oxidoreductase

Query Match      87.1%; Score 27; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      194 TSSRAT 199

RESULT 12
B29606
methylenomycin A resistance protein - Streptomyces coelicolor plasmid SCP1
C:Species: Streptomyces coelicolor
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Sep-1999
C:Accession: B29606
R:Neal, R.J.; Chater, K.F.
Gene 58, 229-241, 1987
A:Title: Nucleotide sequence analysis reveals similarities between proteins determining i
A:Reference number: A91580; MUID:88112873; PMID:2828187
A:Accession: B29606
A:Molecule type: DNA
A:Residues: 1-475 <NEA>
C:Genetics:
A:Gene: mmr
A:Genome: plasmid
A:Superfamily: tetracycline resistance protein
C:Keywords: antibiotic resistance; transmembrane protein

Query Match      87.1%; Score 27; DB 2; Length 475;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATSSRAT 7
DB      204 ATSSRAT 210

RESULT 13
T00404
probable cytochrome P450 At2g44890 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

```


potassium transport protein kup [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C;Accession: AG00001
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, J.
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB00001; MUID:21470413; PMID:11586360
 A;Accession: AG00001
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-622 <KUR>
 A;Cross-references: GB:AL590842; PIDN:CAC88873.1; PID:gl5978121; GSPDB:GN00175
 C;Genetics:
 A;Gene: kup
 Query Match 87.1%; Score 27; DB 2; Length 622;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TSSRAT 7
 DB 94 TSSRAT 99
 Search completed: April 21, 2004, 17:38:30
 Job time : 8.3913 secs

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Feb-2001
 C;Accession: T00404; A84884
 R;Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
 submitted to the EMBL Data Library, July 1997
 A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
 A;Reference number: Z14146
 A;Accession: T00404
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-490 <ROU>
 A;Cross-references: EMBL:AC002388; NID:g3420042; PID:g2344895
 A;Experimental source: Cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84884
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-490 <STO>
 A;Cross-references: GB:AE002093; NID:g2344895; PIDN:AAC31835.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g44890; T13E15.10
 A;Map position: 2
 A;Introns: 33/2; 153/3; 248/3; 361/3; 428/3
 A;Cytrochrome P450 52A3; cytochrome P450 homology
 C;Superfamily: Candida cytochrome P450 homology <P45>
 F;281-456/Domain: cytochrome P450 homology <P45>
 Query Match 87.1%; Score 27; DB 2; Length 490;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATSSRAT 7
 DB 196 ATSSRAT 202

RESULT 14
 AG3470
 Glycerol-3-phosphate dehydrogenase (EC 1.1.1.99.5) [imported] - Brucella melitensis (strain
 C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C;Accession: AG3470
 R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AG3470
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-511 <KUR>
 A;Cross-references: GB:AE008917; PIDN:AAL52930.1; PID:gl7983778; GSPDB:GN00190
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME11749
 A;Map position: 1
 C;Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)
 C;Keywords: oxidoreductase
 Query Match 87.1%; Score 27; DB 2; Length 511;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TSSRAT 7
 DB 55 TSSRAT 60

RESULT 15
 AG0001
 Query Match 87.1%; Score 27; DB 2; Length 511;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TSSRAT 7
 DB 55 TSSRAT 60

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 18.6667 Seconds
(without alignments)

118.319 Million cell updates/sec

Title: SEQ5

Perfect score: 31

Sequence: 1 atserat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	90.3	281	16 Q87CT2	Q87ct2 xylella fas
2	28	90.3	350	2 Q48277	Q48277 haemophilus
3	28	90.3	440	13 Q7T298	Q7t298 brachydanio
4	28	90.3	543	4 Q14879	Q14879 homo sapien
5	28	90.3	693	2 Q50471	Q50471 mycobacteri
6	28	90.3	716	4 Q9NVE4	Q9nye4 homo sapien
7	28	90.3	798	5 Q9U225	Q9u225 caenorhabdi
8	28	90.3	833	5 Q9U016	Q9u016 plasmodium
9	28	90.3	1205	5 Q9V8B7	Q9v8b7 drosophila
10	27	87.1	109	4 Q9UL86	Q9ul86 homo sapien
11	27	87.1	131	17 Q9Y987	Q9y987 aeropyrum p
12	27	87.1	165	4 Q9UD42	Q9ud42 homo sapien
13	27	87.1	201	16 Q8P3G0	Q8p3g0 xanthomonas
14	27	87.1	227	12 Q86620	Q86620 orf virus (
15	27	87.1	228	10 Q9M290	Q9m290 arabidopsis
16	27	87.1	359	10 Q8LPA9	Q8lpa9 hordeum vul

17	27	87.1	379	12 Q8JS35	Q8js35 phthorimaea
18	27	87.1	391	11 Q31ZV1	Q31zv1 rattus norv
19	27	87.1	391	16 Q8EC86	Q8ec86 shewanella
20	27	87.1	401	5 Q95TH7	Q95th7 drosophila
21	27	87.1	430	5 Q7YUZ9	Q7yuz9 trypanosoma
22	27	87.1	490	10 Q22162	Q22162 arabidopsis
23	27	87.1	493	5 Q8SWC5	Q8swc5 encephalito
24	27	87.1	503	12 Q99FW7	Q99fw7 human papil
25	27	87.1	503	16 Q8G2W1	Q8g2w1 bruceella su
26	27	87.1	511	16 Q8YEX8	Q8yex8 bruceella me
27	27	87.1	554	6 Q95L89	Q95l89 bos taurus
28	27	87.1	580	6 Q8WML4	Q8wml4 bos taurus
29	27	87.1	598	4 Q75268	Q75268 homo sapien
30	27	87.1	602	10 Q94DS1	Q94ds1 oryza sativ
31	27	87.1	622	16 Q8ZJT0	Q8zjt0 versinia pe
32	27	87.1	622	11 Q8Z327	Q8z327 rattus norv
33	27	87.1	725	12 Q8QRW1	Q8qrw1 chimpanzee
34	27	87.1	753	2 Q933S4	Q933s4 escherichia
35	27	87.1	753	2 Q93Q52	Q93q52 shigella fi
36	27	87.1	852	10 Q7Y097	Q7y097 oryza sativ
37	27	87.1	863	4 Q8YF21	Q8tf21 homo sapien
38	27	87.1	880	5 Q7YU85	Q7yu85 drosophila
39	27	87.1	882	5 Q9VA36	Q9va36 drosophila
40	27	87.1	927	16 Q861W9	Q861w9 pseudomonas
41	27	87.1	1127	13 Q9PU92	Q9pu92 cyprinus ca
42	27	87.1	1171	5 Q9VTW8	Q9vtw8 drosophila
43	27	87.1	1464	11 Q63728	Q63728 rattus norv
44	27	87.1	1464	11 Q08948	Q08948 rattus norv
45	27	87.1	2012	10 Q8GSW6	Q8gs66 oryza sativ

ALIGNMENTS

RESULT 1

Q87CT2	ID	Q87CT2	PRELIMINARY;	PRT;	281 AA.
AC	Q87CT2;	Q87CT2;			
DT	01-JUN-2003	(TREMBLrel. 24, Created)			
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE		Plasmid-related protein.			
DE		TRAN OR PD0981.			
OS		Xylella fastidiosa (strain Temecula / ATCC 700964).			
OC		Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC		Xanthomonadaceae; Xylella.			
OC		NCBI_TaxID=183190;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RP		MEDLINE=22421331; PubMed=12533478;			
RA		Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,			
RA		Miyaki C.F., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Silva F.R.,			
RA		Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,			
RA		Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Teal S.M.,			
RA		Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,			
RA		Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,			
RA		Maingo C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,			
RA		Baia G.S., Bianco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,			
RA		da Cunha A.F., Penille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,			
RA		Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,			
RA		de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,			
RA		Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,			
RA		Kitajima J.P.;			
RT		"Comparative analyses of the complete genome sequences of Pierce's			
RT		disease and citrus variegated chlorosis strains of Xylella			
RT		fastidiosa." 185:1018-1026(2003).			
RL		J. Bacteriol. 185:1018-1026(2003).			
DR		EMBL; AB012556; AA028843.1; -			
DR		InterPro; IPR006528; PhagesPP1_gp7.			
DR		Pfam; PF04233; Phage_Mu_F; 1.			
KW		Complete proteome.			
SQ		SEQUENCE 281 AA; 31303 MW; 6B7E5544FAEC6A42 CRC64;			

Query Match 90.3%; Score 28; DB 16; Length 281;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 |||||
 Db 196 ATASRAT 202
 |||||

RESULT 2
 Q48277 PRELIMINARY; PRT; 350 AA.
 AC Q48277;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Putative major capsid protein.
 OS Haemophilus somnus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=731;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=HS25;
 RC STRAIN=HS25;
 RA Pontarollo R.A., Rioux C.R., Potter A.A.;
 RX MEDLINE=97221585; PubMed=9088631;
 RT "Cloning and characterization of bacteriophage-like DNA from
 Haemophilus somnus homologous to phages P2 and HP1."
 RL J. Bacteriol. 179:1872-1879 (1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=HS25;
 RC STRAIN=HS25;
 RA Pontarollo R.A.;
 RL Thesis (1996); V. I. D. O., University of Saskatchewan.
 DR EMBL: U28154; AAC45158.1; -
 DR InterPro: IPR006441; Major capsid_p2.
 DR Pfam: PF05125; Phage_cap_P2; 1.
 DR TRIFPAME; TIGR01551; major_capsid_p2; 1.
 SQ SEQUENCE 350 AA; 38973 MW; 07B47EC8F2C86116 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 350;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 |||||
 Db 155 ATSNRAT 161
 |||||

RESULT 3
 Q7T298 PRELIMINARY; PRT; 440 AA.
 AC Q7T298;
 DT 01-OCT-2003 (TREMELrel. 25, Created)
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Spletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Musny D.M., Sodergren S.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Mair M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RC Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC054634; AAH54634.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 440 AA; 49158 MW; 2480B79309437752 CRC64;

Query Match 90.3%; Score 28; DB 13; Length 440;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 |||||
 Db 370 ATSSRST 376
 |||||

RESULT 4
 Q14879 PRELIMINARY; PRT; 543 AA.
 AC Q14879;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Mucin (Fragment).
 GN MUC5B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Tracheobronchial mucosa;
 RX MEDLINE=93343858; PubMed=7916618;
 RA Dufosse J., Porchet N., Audie J.P., Guyonnet Duperrat V., Laine A.,
 RA Van-Seuningen I., Marrakchi S., Degand P., Aubert J.P.;
 RT "Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic
 RT alternating domains in human mucin peptides mapped to 1p15.";
 RL Biochem. J. 293:329-337 (1993).
 DR EMBL: X74370; CAA52408.1; -
 DR FIR; S35047; S35047.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
 DR InterPro: IPR002965; P:rich extensn.
 DR PRINTS: PR01217; PRICHEXTENSN.
 FT NON_TER 1 543
 FT NON_TER 543 543
 SQ SEQUENCE 543 AA; 55197 MW; 6767A5E3518B287B CRC64;

Query Match 90.3%; Score 28; DB 4; Length 543;
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
 |||||
 Db 73 ATSSKAT 79
 |||||

RESULT 5

```

Q50471
ID Q50471 PRELIMINARY; PRT; 693 AA.
AC Q50471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Orf 5, of katG (species-specific fragment) (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=95131752; PubMed=7830574;
RA Zhang Y., Young D.;
RT "Strain variation in the katG region of Mycobacterium tuberculosis."
RL Mol. Microbiol. 14:301-308(1994).
DR EMBL; S77045; AAC60492.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR000183; Decarboxylase2.
DR InterPro; IPR002989; Mycobac_pentapep.
DR Pfam; PF01469; Pentapeptide 2; 8.
DR PROSITE; PS00879; ODR DC 2.2; 3.
FT NON TER 1
FT PROSITE 1
SQ SEQUENCE 693 AA; 68111 MW; BE614BC8B251B24B CRC64;

Query Match 90.3%; Score 28; DB 2; Length 693;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 693 ATSSRAT 689

RESULT 6
Q9NYE4 PRELIMINARY; PRT; 716 AA.
ID Q9NYE4;
AC Q9NYE4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cervical mucin MUC5B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=95131752; PubMed=7830574;
RA Zhang Y., Young D.;
RT "Strain variation in the katG region of Mycobacterium tuberculosis."
RL Mol. Microbiol. 14:301-308(1994).
DR EMBL; S77045; AAC60492.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR000183; Decarboxylase2.
DR InterPro; IPR002989; Mycobac_pentapep.
DR Pfam; PF01469; Pentapeptide 2; 8.
DR PROSITE; PS00879; ODR DC 2.2; 3.
FT NON TER 1
FT PROSITE 1
SQ SEQUENCE 716 AA; 71194 MW; 6F3F20E7512289F3 CRC64;

Query Match 90.3%; Score 28; DB 4; Length 716;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 382 ATSSRAT 388

RESULT 7
Q9U225 PRELIMINARY; PRT; 798 AA.
ID Q9U225;
AC Q9U225;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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```

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Y56A3A.6 protein.
GN Y56A3A.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RA Matthews L.;
RP Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL132860; CAB60515.1; -.
DR WormRep; Y56A3A.6; CR22577;
SQ SEQUENCE 798 AA; 85950 MW; 172FEB04895A9EEB CRC64;

Query Match 90.3%; Score 28; DB 5; Length 798;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 659 ATSSRAT 665

RESULT 8
Q9U016 PRELIMINARY; PRT; 833 AA.
ID Q9U016;
AC Q9U016;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN MAL4P2.35;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Devlin K., Bowman S., Churcher C., Harris B., Harris D., Lawson D.,
RA Quail M., Barrrell B.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035475; CAB62877.2; -.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 100542 MW; DD231B04831DFD74 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 833;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 57 ATSSRAT 63

RESULT 9
Q9V8B7 PRELIMINARY; PRT; 1205 AA.
ID Q9V8B7;
AC Q9V8B7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG5756 protein.
GN CG5756.
OS Drosophila melanogaster (Fruit fly).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brail J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherrry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:12185-2195(2000).
DR EMBL; AE003800; AAF57754.1; -.
DR FlyBase; FBgn0034301; CG5756.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_perA.
DR Pfam; PF01607; CBM_14; 1.
DR SMART; SM00494; ChtBD2; 1.
SQ SEQUENCE 1205 AA; 132314 MW; C18E2F0E0491AF62 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 1205;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 725 ATSSRAT 731

RESULT 10
Q9UL86
ID AC Q9UL86 PRELIMINARY; PRT; 109 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region

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```

DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR PIR; B30607; B30607.
DR PIR; I30501; I30501.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
Db 52 TSSRAT 57

RESULT 11
Q9Y987 PRELIMINARY; PRT; 131 AA.
ID AC Q9Y987
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APE2398.
GN APE2398.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AF000064; BAA81413.1; -.
DR PIR; E72469; E72469.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 131 AA; 13019 MW; 0DA7559BA655BAA1 CRC64;

Query Match 87.1%; Score 27; DB 17; Length 131;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSSRAT 7
Db 38 TSSRAT 43

```

RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463 (2002).

DR EMBL; AL138641; CAB86913.1; --
 DR PIR; T47425; T47425. NAM.
 DR InterPro; IPR003441; NAM.
 DR Pfam; PF02365; NAM; 1.
 SQ SEQUENCE 228 AA; 25304 MW; B5D67E70E96D2F44 CRC64;

Query Match 87.1%; Score 27; DB 10; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TSSRAT 7
 |||||
 Db 175 TSSRAT 180

Search completed: April 21, 2004, 17:37:21
 Job time : 21.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 28 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ5

Perfect score: 31

Sequence: 1 atserat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	31	100.0	88	AAU41616	AAU41616 Propionib
2	31	100.0	88	ABM38135	ABM38135 Propionib
3	31	100.0	474	AAU30724	AAU30724 Arabidops
4	31	100.0	495	AAU30723	AAU30723 Arabidops
5	31	100.0	497	AAU30722	AAU30722 Arabidops
6	31	100.0	501	ADB70174	ADB70174 C. neofor
7	28	90.3	59	AAU41209	AAU41209 Propionib
8	28	90.3	59	ABM37728	ABM37728 Propionib
9	28	90.3	70	AAU66145	AAU66145 Propionib
10	28	90.3	70	AAU50420	AAU50420 Propionib
11	28	90.3	70	ABP03196	ABP03196 Human ORF
12	28	90.3	70	ABM46939	ABM46939 Propionib
13	28	90.3	70	ABM62664	ABM62664 Propionib
14	28	90.3	82	ABP75831	ABP75831 Human sec
15	28	90.3	104	AAU56589	AAU56589 Propionib
16	28	90.3	104	ABM64894	ABM64894 Propionib
17	28	90.3	104	ABM53108	ABM53108 Propionib
18	28	90.3	163	AAU54597	AAU54597 Propionib
19	28	90.3	163	ABM51116	ABM51116 Propionib
20	28	90.3	173	AAU74998	AAU74998 Neisseria
21	28	90.3	173	AAU74997	AAU74997 Neisseria
22	28	90.3	197	AAU74994	AAU74994 Neisseria
23	28	90.3	197	AAU74995	AAU74995 Neisseria
24	28	90.3	251	AAU67887	AAU67887 Propionib
25	28	90.3	251	ABM64406	ABM64406 Propionib

26	28	90.3	363	6	ABM66094	Propionib
27	28	90.3	842	5	ABP73474	Candida a
28	28	90.3	1205	4	ABM61778	Proseophil
29	28	90.3	4315	5	ABP43908	MUC5B par
30	27	87.1	7	5	ABP62365	Human imm
31	27	87.1	10	4	AAU87027	Saccharom
32	27	87.1	10	4	AAU87029	Saccharom
33	27	87.1	61	4	AAU54148	Propionib
34	27	87.1	61	6	ABM50667	Propionib
35	27	87.1	102	4	AAU89514	Human ant
36	27	87.1	102	6	AAE38332	Human ant
37	27	87.1	109	4	AAU62768	Human HIV
38	27	87.1	109	5	ABG92885	Human imm
39	27	87.1	109	6	AAU29549	Human 7.1
40	27	87.1	109	6	ABG71911	Human ant
41	27	87.1	109	6	ADA89184	Human ant
42	27	87.1	120	5	ABP62191	Novel hum
43	27	87.1	178	4	AAU33249	Human sec
44	27	87.1	183	2	AAU29862	Human sec
45	27	87.1	203	2	AAU47336	Peptide f

ALIGNMENTS

RESULT 1
AAU41616
ID AAU41616 standard; protein; 88 AA.
AC AAU41616;
XX
XX
DT 13-FEB-2002 (first entry)
XX
XX
DE Propionibacterium acnes immunogenic protein #2512.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WC200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WC-US012865.

XX 21-APR-2000; 2000US-0199047P.

XX 02-JUN-2000; 2000US-0208941P.

XX 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59515.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

XX vaccinating against and diagnosing infections, especially useful for

XX treating acne vulgaris.

XX Example 1; SEQ ID NO 2811; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

XX polypeptides. The proteins and their associated DNA sequences are used in

XX the treatment, prevention and diagnosis of medical conditions caused by

XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

XX P. acnes is also involved in infections of bone, joints and the central

XX nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 88 AA;
 SQ

Query Match 100.0%; Score 31; DB 4; Length 88;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSRAT 7
 Db 75 ATSSSRAT 81
 |||||

RESULT 2
 ABM38135
 ID ABM38135 standard; protein; 88 AA.
 AC ABM38135;
 DT 20-OCT-2003 (first entry)
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #2811.
 XX
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 OS
 OS Propionibacterium acnes.
 XX
 XX WO2003033515-A1.
 XX
 XX 24-APR-2003.
 XX
 XX 11-OCT-2002; 2002WO-US032727.
 XX
 XX 15-OCT-2001; 2001US-00978825.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 FI Zhang Y, Wang S, Jen S, Lodes MU, Benson DR, Jones R, Carter D;
 FI Barth B, Vallie-Douglass J;
 XX
 XX WPI; 2003-381789/36.
 DR
 DR N-PSDB; ACF64444.
 XX
 XX
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX Example 1; SEQ ID NO 2811; 1481bp; English.
 PS
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 XX encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,

CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 88 AA;
 SQ

Query Match 100.0%; Score 31; DB 6; Length 88;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSSRAT 7
 Db 75 ATSSSRAT 81
 |||||

RESULT 3
 AAG30724
 ID AAG30724 standard; protein; 474 AA.
 XX
 XX AAG30724;
 XX
 XX 17-OCT-2000 (first entry)
 DT
 XX
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 36783.
 DE
 XX
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 XX Arabidopsis thaliana.
 OS
 XX
 XX EP1033405-A2.
 XX
 XX 06-SEP-2000.
 PD
 XX
 XX 25-FEB-2000; 2000EP-00301439.
 PF
 XX
 XX 25-FEB-1999; 99US-0121825P.
 PR
 XX 05-MAR-1999; 99US-0123180P.
 PR
 XX 09-MAR-1999; 99US-0123548P.
 PR
 XX 23-MAR-1999; 99US-0125788P.
 PR
 XX 25-MAR-1999; 99US-0126264P.
 PR
 XX 29-MAR-1999; 99US-0126785P.
 PR
 XX 01-APR-1999; 99US-0127462P.
 PR
 XX 06-APR-1999; 99US-0128234P.
 PR
 XX 08-APR-1999; 99US-0128714P.
 PR
 XX 16-APR-1999; 99US-0129845P.
 PR
 XX 19-APR-1999; 99US-0130077P.
 PR
 XX 21-APR-1999; 99US-0130449P.
 PR
 XX 23-APR-1999; 99US-0130510P.
 PR
 XX 28-APR-1999; 99US-0130891P.
 PR
 XX 30-APR-1999; 99US-0131449P.
 PR
 XX 30-APR-1999; 99US-0132048P.
 PR
 XX 30-APR-1999; 99US-0132407P.
 PR
 XX 04-MAY-1999; 99US-0132484P.
 PR
 XX 05-MAY-1999; 99US-0132485P.
 PR
 XX 06-MAY-1999; 99US-0132486P.
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 XX 06-MAY-1999; 99US-0132487P.
 PR
 XX 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134376P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR	14-JUL-1999;	99US-0143624P.	PR	08-OCT-1999;	99US-0158232P.
PR	15-JUL-1999;	99US-0144005P.	PR	12-OCT-1999;	99US-0158369P.
PR	16-JUL-1999;	99US-0144085P.	PR	13-OCT-1999;	99US-0159293P.
PR	16-JUL-1999;	99US-0144086P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144325P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144331P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144332P.	PR	14-OCT-1999;	99US-0159330P.
PR	19-JUL-1999;	99US-0144333P.	PR	14-OCT-1999;	99US-0159331P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159637P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159638P.
PR	20-JUL-1999;	99US-0144352P.	PR	18-OCT-1999;	99US-0159584P.
PR	20-JUL-1999;	99US-0144632P.	PR	21-OCT-1999;	99US-0160741P.
PR	20-JUL-1999;	99US-0144884P.	PR	21-OCT-1999;	99US-0160767P.
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0160768P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160770P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160815P.
PR	22-JUL-1999;	99US-0145089P.	PR	22-OCT-1999;	99US-0160980P.
PR	22-JUL-1999;	99US-0145192P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160989P.
PR	23-JUL-1999;	99US-0145218P.	PR	25-OCT-1999;	99US-0161404P.
PR	23-JUL-1999;	99US-0145224P.	PR	25-OCT-1999;	99US-0161405P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145913P.	PR	26-OCT-1999;	99US-0161359P.
PR	27-JUL-1999;	99US-0145918P.	PR	26-OCT-1999;	99US-0161360P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161361P.
PR	28-JUL-1999;	99US-0145951P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146386P.	PR	28-OCT-1999;	99US-0161992P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161993P.
PR	03-AUG-1999;	99US-0147038P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147204P.			
PR	04-AUG-1999;	99US-0147302P.			
PR	05-AUG-1999;	99US-0147192P.			

Query Match 100.0%; Score 31; DB 3; Length 497;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
|||||
377 ATSSRAT 383

Db

RESULT 6
ADB70174
ID ADB70174 standard; protein; 501 AA.
XX
AC ADB70174;
XX
XX
DT 04-DEC-2003 (first entry)
XX
DE C. neoformans amino acid sequence SEQ ID NO:3218.
XX
XX fungicide; gene therapy; infection.
KW Cryptococcus neoformans.
XX
OS Cryptococcus neoformans.
XX
PN WO2003052076-A2.
XX
PD 26-JUN-2003.
XX
PF 17-DEC-2002; 2002WO-US040225.
XX
PR 17-DEC-2001; 2001US-0341261P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Zamudio C, Eroshkin AM;
XX
XX WPI; 2003-533017/50.
DR N-PSDB; ADB69091.
XX
XX New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
PT
PT Claim 9; SEQ ID NO 3218; 136pp; English.
XX
XX The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A CC
CC polynucleotide of the invention has fungicide activity, and may have a CC
CC use in gene therapy. The nucleic acid is useful for preparing a CC
CC composition for treating an infection caused by Cryptococcus neoformans. CC
CC The present sequence represents a C. neoformans sequence of the CC
CC invention. Note: The sequence data for this patent is not represented in CC
CC the printed specification, but was obtained in electronic format directly CC
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 501 AA;

Query Match 100.0%; Score 31; DB 7; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
|||||
47 ATSSRAT 53

Db

RESULT 7
AAU41209
ID AAU41209 standard; protein; 59 AA.
XX
AC AAU41209;
XX
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #2105.

Best Local Similarity 100.0%; Score 28; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
|||||
27 ATASRAT 33

Db

RESULT 8
ABM37728
ID ABM37728 standard; protein; 59 AA.
XX
AC ABM37728;
XX
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #2404.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
uvelitis; endophthalmitis; bone; joint; central nervous system; ELISA;
inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
dermatological; osteopathic; neuroprotectant.
Propionibacterium acnes.
WO200181581-A2.
01-NOV-2001.
20-APR-2001; 2001WO-US012865.
21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
(CORI-) CORIXA CORP.
Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
L'maisonneuve J, Zhang Y, Jen S, Carter D;
WPI; 2001-616774/71.
N-PSDB; AAS59514.
Propionibacterium acnes polypeptides and nucleic acids useful for
treating acne vulgaris.
Example 1; SEQ ID NO 2404; 1069pp; English.
Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
polypeptides. The proteins and their associated DNA sequences are used in
the treatment, prevention and diagnosis of medical conditions caused by
P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
P. acnes is also involved in infections of bone, joints and the central
nervous system, however it is particularly involved in the inflammatory
lesions associated with acne vulgaris. A method for detecting the
presence or absence of P. acnes in a patient comprises contacting a
sample with a binding agent that binds to the proteins of the invention
and determining the amount of bound protein in the sample. The
polypeptides may be used as antigens in the production of antibodies
specific for P. acnes proteins. These antibodies can be used to
downregulate expression and activity of P. acnes polypeptides and
therefore treat P. acnes infections. The antibodies may also be used as
diagnostic agents for determining P. acnes presence, for example, by
enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
this patent did not form part of the printed specification, but was
obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pat_sequences

XX Acne vulgaris; antisborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX Propionibacterium acnes.
 XX WO2003033515-A1.
 XX 24-APR-2003.
 XX 11-OCT-2002; 2002WO-US032727.
 XX 15-OCT-2001; 2001US-00978825.
 XX (CORI-) CORIXA CORP.
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglas J;
 XX WPI; 2003-381789/36.
 DR N-PSDB; ACF64443.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX Example 1; SEQ ID NO 2404; 1481pp; English.
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 59 AA;
 Query Match 90.3%; Score 28; DB 6; Length 59;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSRAT 7
 DB 27 ATASRAT 33
 RESULT 9
 AAU66145
 ID AAU66145 standard; protein; 70 AA.
 XX
 AC AAU66145;

XX Sequence 70 AA;
 Query Match 90.3%; Score 28; DB 4; Length 70;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSRAT 7
 DB 3 ATSSRAT 9
 RESULT 10
 AAU50420
 ID AAU50420 standard; protein; 70 AA.
 XX
 AC AAU50420;

XX 27-FEB-2002 (first entry)
 XX Propionibacterium acnes immunogenic protein #27041.
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX Propionibacterium acnes.
 XX WO200181581-A2.
 XX 01-NOV-2001.
 XX 20-APR-2001; 2001WO-US012865.
 XX 21-APR-2000; 2000US-019047P.
 XX 02-JUN-2000; 2000US-0208841P.
 XX 07-JUL-2000; 2000US-0216747P.
 XX (CORI-) CORIXA CORP.
 XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59715.
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX Example 1; SEQ ID NO 27340; 1069pp; English.
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, uveitis,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 70 AA;
 Query Match 90.3%; Score 28; DB 4; Length 70;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATSSRAT 7
 DB 3 ATSSRAT 9
 RESULT 10
 AAU50420
 ID AAU50420 standard; protein; 70 AA.
 XX
 AC AAU50420;

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XX DT 27-FEB-2002 (first entry)
XX DE Propionibacterium acnes immunogenic protein #11316.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS Propionibacterium acnes.
XX PN WO200181581-A2.
XX PD 01-NOV-2001.
XX EF 20-APR-2001; 2001WO-US012865.
XX PR 21-APR-2000; 2000US-0199047P.
XX PR 02-JUN-2000; 2000US-0208841P.
XX PR 07-JUL-2000; 2000US-0216747P.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX DR N-PSDB; AAS59548.
XX DR WPI; 2001-616774/71.
XX DR N-PSDB; AAS59548.
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.
XX PS Example 1; SEQ ID NO 11615; 1069pp; English.
XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory
XX CC lesions associated with acne vulgaris. A method for detecting the
XX CC presence or absence of P. acnes in a patient comprises contacting a
XX CC sample with a binding agent that binds to the proteins of the invention
XX CC and determining the amount of bound protein in the sample. The
XX CC polypeptides may be used as antigens in the production of antibodies
XX CC specific for P. acnes proteins. These antibodies can be used to
XX CC downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence, for example, by
XX CC enzyme linked immunosorbent assay (ELISA). Note: the sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 70 AA;
XX
XX Query Match 90.3%; Score 28; DB 4; Length 70;
XX Best Local Similarity 85.7%; Pred. No. 72;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ATSSSRAT 7
XX Db 3 ATSSSRST 9
XX
XX RESULT 11
XX ABP03196
XX ID ABP03196 standard; protein; 70 AA.
XX XX
XX AC ABP03196;

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XX DT 24-JUN-2002 (first entry)
XX DE Human ORFX protein sequence SEQ ID NO:6374.
XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
XX KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX KW hypertension; hypothyroidism; cholesterol ester storage disease;
XX KW immune deficiency; immune disorder; infectious disease;
XX KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX KW myasthenia gravis.
XX OS Homo sapiens.
XX PN WO200192523-A2.
XX PD 06-DEC-2001.
XX PF 29-MAY-2001; 2001WO-US010836.
XX PR 30-MAY-2000; 2000US-0206132P.
XX PR 29-AUG-2000; 2000US-0228716P.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach MD;
XX PI WPI; 2002-106308/14.
XX DR N-PSDB; ABN18948.
XX DR Novel human polypeptides and polynucleotides useful for diagnosing,
XX PT preventing and treating cardiovascular disease, neurodegenerative,
XX PT hyperproliferative disorders and autoimmune disorders.
XX PS Disclosure; SEQ ID NO 6374; 1037pp; English.
XX CC The present invention describes substantially purified human proteins
XX CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX CC in the specification). ABN15762 to ABN27452 encode the human ORFX
XX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX CC treating or preventing a pathology associated with an ORFX-associated
XX CC disorder in humans, and in the manufacture of a medicament for treating a
XX CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX CC sequences can be used in gene therapy. ORFX sequences can be used in the
XX CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
XX CC osteoarthritis, neurodegenerative disorders, disorders related to organ
XX CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
XX CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
XX CC storage disease, various immune deficiencies and disorders, infectious
XX CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
XX CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
XX CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
XX CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
XX CC bone degenerative disorders, or periodontal disease, and for gut
XX CC protection or regeneration and treatment of lung or liver fibrosis,
XX CC reperfusion injury in various tissues and conditions resulting from
XX CC systemic cytokine damage. N.B. The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 70 AA;
XX
XX Query Match 90.3%; Score 28; DB 5; Length 70;
XX Best Local Similarity 85.7%; Pred. No. 72;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ATSSSRAT 7
XX Db 3 ATSSSRST 9
XX
XX RESULT 7
XX ABP03196
XX ID ABP03196 standard; protein; 70 AA.
XX XX
XX AC ABP03196;

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RESULT 12
ABM46939
XX ABM46939 standard; protein; 70 AA.
XX AC
XX ABM46939;
XX 20-OCT-2003 (first entry)
XX DE
XX Propionibacterium acnes predicted ORF-encoded polypeptide #11615.
XX KW
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX OS
XX Propionibacterium acnes.
XX PN WO2003033515-A1.
XX XX
XX 24-APR-2003.
XX PD
XX 11-OCT-2002; 2002WO-US032727.
XX PF
XX 15-OCT-2001; 2001US-00978825.
XX PR
XX (CORI-) CORIXA CORP.
XX PA
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieue-Douglas J;
XX WPI; 2003-381789/36.
XX DR N-PSDB; ACF64477.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
XX Example 1; SEQ ID NO 11615; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC polynucleotide of the invention; a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 70 AA;
XX
XX Query Match 90.3%; Score 28; DB 6; Length 70;
XX Best Local Similarity 85.7%; Pred. No. 72;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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Query Match          90.3%; Score 28; DB 6; Length 70;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 3 ATSSRST 9

RESULT 14
ABP75831
ID ABP75831 standard; protein; 82 AA.
XX
AC ABP75831;
XX
DT 10-FEB-2003 (first entry)
XX
DE Human secretory polypeptide SPTM SEQ ID NO 1015.
XX
KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
KW anti-inflammatory; immunosuppressive; neuroprotective; neoplastic;
KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
KW secretory polynucleotide; secretory protein.
XX
OS Homo sapiens.
XX
FN WO200283876-A2.
XX
PD 24-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US009921.
XX
PR 29-MAR-2001; 2001US-0280067P.
XX
PR 29-MAR-2001; 2001US-0280068P.
XX
PR 16-MAY-2001; 2001US-0291280P.
XX
PR 17-MAY-2001; 2001US-0291829P.
XX
PR 17-MAY-2001; 2001US-0291849P.
XX
PR 19-JUN-2001; 2001US-0299428P.
XX
PR 20-JUN-2001; 2001US-0299778P.
XX
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
WPI; 2003-075543/07.
DR N-PSDB; AB236273.
XX
XX New human secretory proteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
PT cancers.
XX
PS Claim 27; SEQ ID NO 1015; 458pp + Sequence Listing; English.
XX
XX The invention relates to a secretory polynucleotide (designated sptm)
CC comprising any of 567 polynucleotide sequences (AB235837-AB236403), a
CC naturally occurring polynucleotide sequence at least 90 % identical to
CC the polynucleotide sequence, a polynucleotide complementary to them or an
CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
CC treating, preventing or diagnosing a disease or condition associated with
CC the expression of functional SPTM. These are particularly useful for
CC diagnosing, treating or preventing autoimmune/inflammatory disorders
CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,

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CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). The present sequence is one of the SPTM
CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 82 AA;
Query Match          90.3%; Score 28; DB 6; Length 82;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
DB 74 ATSSKAT 80
|||||

RESULT 15
AAU56589
ID AAU56589 standard; protein; 104 AA.
XX
AC AAU56589;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #17485.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
FN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
XX
PR 02-JUN-2000; 2000US-0208841P.
XX
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
WPI; 2001-616774/71.
DR N-PSDB; AAS59577.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 1784; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention

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CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 104 AA;
Query Match 90.3%; Score 28; DB 4; Length 104;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATSSRAT 7
|||:|
Db 45 ATSSKAT 51

Search completed: April 21, 2004, 17:33:15
Job time : 31 secs

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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 21.1014 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ5
Perfect score: 31
Sequence: 1 atssrat 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	96	14	US-10-041-860-377
2	31	100.0	108	14	US-10-041-860-49
3	31	100.0	108	14	US-10-041-860-225
4	31	100.0	108	14	US-10-041-860-259
5	31	100.0	108	14	US-10-041-860-375
6	31	100.0	140	12	US-10-424-599-176884
7	31	100.0	497	16	US-10-389-566-2341
8	31	100.0	501	15	US-10-320-797-3218
9	28	90.3	340	12	US-10-425-114-41459
10	28	90.3	842	14	US-10-032-585-7311
11	27	87.1	79	12	US-10-424-599-148739
12	27	87.1	96	14	US-10-041-860-376
13	27	87.1	109	12	US-10-371-942-28
14	27	87.1	109	14	US-10-067-800-62
15	27	87.1	109	15	US-10-292-486-47

16	27	87.1	212	14	US-10-006-593-118	Sequence 118, App
17	27	87.1	212	15	US-10-307-724-118	Sequence 118, App
18	27	87.1	245	14	US-10-128-714-3428	Sequence 3428, App
19	27	87.1	245	15	US-10-369-493-3216	Sequence 3216, App
20	27	87.1	263	15	US-10-422-628-14	Sequence 14, Appl
21	27	87.1	269	12	US-10-425-114-50879	Sequence 50879, A
22	27	87.1	331	15	US-10-327-413-2	Sequence 2, Appl
23	27	87.1	345	14	US-10-128-714-8428	Sequence 8428, App
24	27	87.1	501	12	US-10-424-599-192945	Sequence 192945, A
25	27	87.1	722	12	US-10-282-122A-77710	Sequence 77710, A
26	27	87.1	752	15	US-10-104-047-1975	Sequence 1975, App
27	27	87.1	753	14	US-10-238-075-1277	Sequence 1277, App
28	27	87.1	777	14	US-10-208-219-93	Sequence 93, Appl
29	27	87.1	988	9	US-09-843-676-69	Sequence 69, Appl
30	27	87.1	988	9	US-09-766-253-69	Sequence 69, Appl
31	27	87.1	988	10	US-09-438-486-69	Sequence 69, Appl
32	27	87.1	988	12	US-10-325-810-112	Sequence 112, App
33	27	87.1	988	14	US-10-053-758-69	Sequence 69, Appl
34	27	87.1	988	14	US-10-054-295-69	Sequence 69, Appl
35	27	87.1	988	14	US-10-054-611-69	Sequence 69, Appl
36	27	87.1	988	14	US-10-044-692-112	Sequence 112, App
37	27	87.1	988	14	US-10-044-539-112	Sequence 112, App
38	27	87.1	1153	9	US-09-992-056-2	Sequence 2, Appl
39	27	87.1	1153	12	US-10-220-282A-2	Sequence 2, Appl
40	27	87.1	1153	14	US-10-224-249-13	Sequence 13, Appl
41	27	87.1	1464	10	US-09-934-070-15	Sequence 15, Appl
42	27	87.1	1464	10	US-09-922-011-1	Sequence 1, Appl
43	27	87.1	1464	12	US-10-222-772-15	Sequence 15, Appl
44	26	83.9	34	14	US-10-218-102-255	Sequence 255, App
45	26	83.9	65	12	US-10-424-599-158367	Sequence 158367, A

ALIGNMENTS

RESULT 1
US-10-041-860-377
; Sequence 377, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 377
; LENGTH: 96
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-377

Query Match 100.0%; Score 31; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 51 ATSSRAT 57

RESULT 2
US-10-041-860-49
; Sequence 49, Application US/10041860

Publication No. US20030157109A1
 GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.
 APPLICANT: Jia, Xiao-Chi
 APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezabeh, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 49
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-49

Query Match 100.0%; Score 31; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 Db 51 ATSSRAT 57

RESULT 3
 US-10-041-860-225
 Sequence 225, Application US/10041860
 Publication No. US20030157109A1
 GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.
 APPLICANT: Jia, Xiao-Chi
 APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezabeh, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 225
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-225

Query Match 100.0%; Score 31; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 Db 51 ATSSRAT 57

RESULT 4
 US-10-041-860-259
 Sequence 259, Application US/10041860
 Publication No. US20030157109A1
 GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi
 APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezabeh, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 259
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-259

Query Match 100.0%; Score 31; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 Db 51 ATSSRAT 57

RESULT 5
 US-10-041-860-375
 Sequence 375, Application US/10041860
 Publication No. US20030157109A1
 GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.
 APPLICANT: Jia, Xiao-Chi
 APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezabeh, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 375
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-375

Query Match 100.0%; Score 31; DB 14; Length 108;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
 Db 51 ATSSRAT 57

RESULT 6
 US-10-424-599-176884
 Sequence 176884, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei

```
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 176884
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130743C.1.pep
US-10-424-599-176884

Query Match          100.0%; Score 31; DB 12; Length 140;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 21 ATSSRAT 27

RESULT 7
US-10-389-566-2341
; Sequence 2341, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2341
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-389-566-2341

Query Match          100.0%; Score 31; DB 16; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 377 ATSSRAT 383

RESULT 8
US-10-320-797-3218
; Sequence 3218, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Ercoshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 3218
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (435)..(435)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (437)..(438)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (429)..(429)
; OTHER INFORMATION: Xaa = any amino acid
US-10-320-797-3218

Query Match          100.0%; Score 31; DB 15; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 47 ATSSRAT 53

RESULT 9
US-10-425-114-41459
; Sequence 41459, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41459
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB075-022-A3_FLI.pep
US-10-425-114-41459

Query Match          90.3%; Score 28; DB 12; Length 340;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 254 ATSSRAT 260

RESULT 10
US-10-032-585-7311
; Sequence 7311, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
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; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7311
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7311

Query Match      90.3%; Score 28; DB 14; Length 842;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSRAT 7
DB      482 STSSRAT 488

RESULT 11
US-10-424-599-148739
; Sequence 148739, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 148739
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105333C.1.bep
US-10-424-599-148739

Query Match      87.1%; Score 27; DB 12; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      17 TSSRAT 22

RESULT 12
US-10-041-860-376
; Sequence 376, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvatan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-62

Query Match      87.1%; Score 27; DB 12; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      52 TSSRAT 57

RESULT 13
US-10-371-942-28
; Sequence 28, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-28

Query Match      87.1%; Score 27; DB 12; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
DB      52 TSSRAT 57

RESULT 14
US-10-067-800-62
; Sequence 62, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-62

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Query Match      87.1%; Score 27; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
Db      52 TSSRAT 57

RESULT 15
US-10-292-486-47
; Sequence 47, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PFS32PI
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 47
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-47

Query Match      87.1%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
Db      52 TSSRAT 57
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Search completed: April 21, 2004, 18:02:07
Job time : 22.1014 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2004, 17:37:29 ; Search time 27.1304 Seconds
(without alignments)
91.715 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 QYGVSSPCS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues 1133595

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Post-processing: Minimum Match 0%
Maximum Match 100%
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ALIGNMENTS

RESULT 1
US-10-041-860-49
; Sequence 49, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

Query Match 100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGVSSPCS 9
| | | | | | | | | |
Db 90 QYGVSSPCS 98

RESULT 2
US-10-041-860-225
; Sequence 225, Application US/10041860

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; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-225

Query Match      100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QYGGSSPCS 9
DB      90 QYGGSSPCS 98

RESULT 3
US-10-041-860-259
; Sequence 259, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-259

Query Match      100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QYGGSSPCS 9
DB      90 QYGGSSPCS 98

RESULT 4
US-10-041-860-375
; Sequence 375, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-375

Query Match      100.0%; Score 51; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QYGGSSPCS 9
DB      90 QYGGSSPCS 98

RESULT 5
US-10-104-047-3475
; Sequence 3475, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: HI-A0105
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3475
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-3475

Query Match      76.5%; Score 39; DB 15; Length 412;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYGGSSPCS 9
DB      93 RYGTSPCS 100

RESULT 6
US-10-013-310-3
; Sequence 3, Application US/10013310
; Publication No. US20020192216A1
; GENERAL INFORMATION:
; APPLICANT: Lamb, Jonathon Robert
; APPLICANT: Hoyne, Gerard Francis
; APPLICANT: Dallman, Margaret Jane
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: 674525-2003
; CURRENT APPLICATION NUMBER: US/10/013,310
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/GB00/02191
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: UK 9913350.6

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; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: UK 9921953.7
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 695
; TYPE: PRT
; ORGANISM: House Mouse
US-10-013-310-3

Query Match      76.5%; Score 39; DB 13; Length 695;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 9
Db 376 RYGTSPCS 383

RESULT 7
US-09-903-248-5
; Sequence 5, Application US/09903248
; Patent No. US20020102263A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV5
; CURRENT APPLICATION NUMBER: US/09/903,248
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-248-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 8
US-09-859-604-5
; Sequence 5, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M
; APPLICANT: Deutch, Alan H
; APPLICANT: Ghanbari, Hossein A
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 CIP
; CURRENT APPLICATION NUMBER: US/09/859,604
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-248-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 9
US-09-903-063-5
; Sequence 5, Application US/09903063
; Patent No. US20020114810A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV3
; CURRENT APPLICATION NUMBER: US/09/903,063
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-063-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 10
US-09-903-216-5
; Sequence 5, Application US/09903216
; Patent No. US20020114811A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV2
; CURRENT APPLICATION NUMBER: US/09/903,216
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-216-5

Query Match      76.5%; Score 39; DB 9; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436
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RESULT 11
 US-09-903-199-5
 ; Sequence 5, Application US/09903199
 ; Patent No. US20020122802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wands, Jack R.
 ; APPLICANT: de la Monte, Suzanne M.
 ; APPLICANT: Ince, Nedim
 ; APPLICANT: Carlson, Rolf I.
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
 ; FILE REFERENCE: 21486-032 DIV4
 ; CURRENT APPLICATION NUMBER: US/09/903,199
 ; CURRENT FILING DATE: 2001-07-11
 ; PRIOR APPLICATION NUMBER: 09/436,184
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-903-199-5

Query Match 76.5%; Score 39; DB 9; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
 :|||||
 Db 430 EYGSPPC 436

RESULT 12
 US-09-903-023-5
 ; Sequence 5, Application US/09903023
 ; Patent No. US20020146421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wands, Jack R.
 ; APPLICANT: de la Monte, Suzanne M.
 ; APPLICANT: Ince, Nedim
 ; APPLICANT: Carlson, Rolf I.
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
 ; FILE REFERENCE: 21486-032 DIV1
 ; CURRENT APPLICATION NUMBER: US/09/903,023
 ; CURRENT FILING DATE: 2001-10-11
 ; PRIOR APPLICATION NUMBER: 09/436,184
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-903-023-5

Query Match 76.5%; Score 39; DB 9; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
 :|||||
 Db 430 EYGSPPC 436

RESULT 13
 US-09-436-184-5
 ; Sequence 5, Application US/09436184
 ; Publication No. US20030031670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wands, Jack R.
 ; APPLICANT: de la Monte, Suzanne M.

; APPLICANT: Ince, Nedim
 ; APPLICANT: Carlson, Rolf I.
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
 ; FILE REFERENCE: R.I. Hosp. - Malignant Neoplasms
 ; CURRENT APPLICATION NUMBER: US/09/436,184
 ; CURRENT FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-436-184-5

Query Match 76.5%; Score 39; DB 10; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
 :|||||
 Db 430 EYGSPPC 436

RESULT 14
 US-10-085-027-1
 ; Sequence 1, Application US/10085027
 ; Publication No. US20020132759A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAZAKI, YOSHIO
 ; APPLICANT: ASANO, TOMOICHIRO
 ; APPLICANT: KUBO, HIDEO
 ; APPLICANT: KANDA, AKIRA
 ; TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
 ; FILE REFERENCE: 4895-0019-0PCT
 ; CURRENT APPLICATION NUMBER: US/10/085,027
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: 09/508,691
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04293
 ; PRIOR FILING DATE: 1998-09-25
 ; PRIOR APPLICATION NUMBER: JP9-263719
 ; PRIOR FILING DATE: 1997-09-29
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-085-027-1

Query Match 76.5%; Score 39; DB 13; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
 :|||||
 Db 430 EYGSPPC 436

RESULT 15
 US-10-334-143-10
 ; Sequence 10, Application US/10334143
 ; Publication No. US20040009549A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
 ; APPLICANT: SUDARSANAM, SUCHA
 ; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
 ; FILE REFERENCE: 038602/1543
 ; CURRENT APPLICATION NUMBER: US/10/334,143
 ; CURRENT FILING DATE: 2002-12-31
 ; PRIOR APPLICATION NUMBER: 60/343,169
 ; PRIOR FILING DATE: 2001-12-31

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; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-10

Query Match      76.5%; Score 39; DB 15; Length 1316;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QYSSPC 8
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Db      504 EYSSPC 510

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Title: SEQ5

Perfect score: 31

Sequence: 1 atsrat 7

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Maximum DB seq length: 2000000000

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Maximum Match 100%

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SUMMARIES

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3	28	90.3	141	4	US-09-252-991A-18631
4	28	90.3	155	4	US-09-252-991A-31910
5	28	90.3	262	4	US-09-252-991A-17126
6	28	90.3	270	4	US-09-252-991A-22477
7	28	90.3	427	4	US-09-252-991A-19612
8	27	87.1	203	1	US-08-063-552-6
9	27	87.1	203	5	PCT-US93-05704-6
10	27	87.1	219	4	US-09-621-976-4221
11	27	87.1	497	4	US-09-252-991A-30856
12	27	87.1	988	3	US-08-851-843A-69
13	27	87.1	988	3	US-08-974-549A-112
14	27	87.1	988	3	US-08-854-050-69
15	27	87.1	988	4	US-09-430-323-69
16	27	87.1	988	4	US-08-912-951-112
17	27	87.1	988	4	US-09-402-181B-112
18	27	87.1	988	4	US-09-721-458-112
19	27	87.1	1146	3	US-09-126-109-12
20	27	87.1	1153	1	US-08-314-917-2
21	27	87.1	1153	1	US-08-265-046-2
22	27	87.1	1153	2	US-08-465-523-2
23	27	87.1	1153	4	US-09-661-258-4
24	27	87.1	1153	5	PCT-US93-11401-2
25	27	87.1	1153	5	PCT-US95-07849-2
26	27	87.1	1464	1	US-08-026-138E-1
27	26	83.9	141	4	US-09-252-991A-25325

28	26	83.9	148	4	US-09-252-991A-16783	Sequence 16783, A
29	26	83.9	150	4	US-09-252-991A-31728	Sequence 31728, A
30	26	83.9	169	4	US-09-252-991A-24301	Sequence 24301, A
31	26	83.9	189	4	US-09-252-991A-32376	Sequence 32376, A
32	26	83.9	262	4	US-09-252-991A-28282	Sequence 28282, A
33	26	83.9	277	4	US-09-252-991A-28460	Sequence 28460, A
34	26	83.9	426	4	US-09-252-991A-18298	Sequence 18298, A
35	26	83.9	536	4	US-09-252-991A-20771	Sequence 20771, A
36	26	83.9	611	4	US-09-252-991A-32402	Sequence 32402, A
37	26	83.9	635	4	US-09-252-991A-33100	Sequence 33100, A
38	26	83.9	856	4	US-09-699-266A-13	Sequence 13, Appl
39	25	80.6	52	1	US-08-361-920-17	Sequence 17, Appl
40	25	80.6	52	1	US-08-479-939-17	Sequence 17, Appl
41	25	80.6	52	1	US-08-483-432-17	Sequence 17, Appl
42	25	80.6	75	4	US-09-345-238B-101	Sequence 101, Appl
43	25	80.6	85	4	US-09-732-210-42	Sequence 42, Appl
44	25	80.6	111	4	US-09-252-991A-17821	Sequence 17821, A
45	25	80.6	138	4	US-09-252-991A-30362	Sequence 30362, A

ALIGNMENTS

RESULT 1
US-09-252-991A-28404
; Sequence 28404, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28404
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28404

Query Match 90.3%; Score 28; DB 4; Length 115;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATSRAT 7
Db 99 ATSRAT 105

RESULT 2
US-09-252-991A-17444
; Sequence 17444, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17444
; LENGTH: 138
; TYPE: PRT

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17444

Query Match          90.3%; Score 28; DB 4; Length 138;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 80 ATSRAT 86

RESULT 3
US-09-252-991A-18631
; Sequence 18631, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18631
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18631

Query Match          90.3%; Score 28; DB 4; Length 141;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 41 STSRAT 47

RESULT 4
US-09-252-991A-31910
; Sequence 31910, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31910
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31910

Query Match          90.3%; Score 28; DB 4; Length 155;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 101 ATSRAT 107

RESULT 5
US-09-252-991A-17126
; Sequence 17126, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17126
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17126

Query Match          90.3%; Score 28; DB 4; Length 262;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 37 ATSRAT 43

RESULT 6
US-09-252-991A-22477
; Sequence 22477, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22477
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22477

Query Match          90.3%; Score 28; DB 4; Length 270;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATSSRAT 7
Db 1 ATSRAT 7

RESULT 7
US-09-252-991A-19612
; Sequence 19612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

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;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 19612
;; LENGTH: 427
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19612

Query Match 90.3%; Score 28; DB 4; Length 427;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 420 STSSRAT 426

RESULT 8

US-08-063-552-6
; Sequence 6, Application US/08063552
; Patent No. 568936
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063,552
FILING DATE: 19930514
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces plasmid
US-08-063-552-6

Query Match 87.1%; Score 27; DB 1; Length 203;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 ATSSRAT 7
Db 194 ATSSRAT 200

RESULT 9

PCT-US93-05704-6
; Sequence 6, Application PC/TUS9305704
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05704
FILING DATE: 19930611
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Streptomyces plasmid
PCT-US93-05704-6

Query Match 87.1%; Score 27; DB 5; Length 203;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATSSRAT 7
Db 194 ATSSRAT 200

RESULT 10

US-09-621-976-4221
; Sequence 4221, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PE2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4221
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16..-1
; NAME/KEY: UNSURE


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; LOCATION: 57
; OTHER INFORMATION: Xaa = Asp.Gly
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Cys.Ser
US-09-821-976-4221

Query Match      87.1%; Score 27; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TSSRAT 7
Db      196 TSSRAT 201

RESULT 11
US-09-252-991A-30856
; Sequence 30856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30856
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30856

Query Match      87.1%; Score 27; DB 4; Length 497;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATSSRAT 7
Db      457 ATSSRAS 463

RESULT 12
US-08-851-843A-69
; Sequence 69, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

US-08-851-843A-69
; Sequence 69, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-851-843A-69

Query Match      87.1%; Score 27; DB 3; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATSSRAT 7
Db      626 ATSDRAT 632

RESULT 13
US-08-974-549A-112
; Sequence 112, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-549A-112

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Query Match      87.1%; Score 27; DB 3; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ATSSRAT 7
Db      626 ATSDRAT 632

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RESULT 14
US-08-854-050-69
; Sequence 69, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-854-050-69

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Query Match      87.1%; Score 27; DB 3; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ATSSRAT 7
Db      626 ATSDRAT 632

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RESULT 15
US-09-430-323-69
; Sequence 69, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:

```

```

; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
;
US-09-430-323-69

Query Match      87.1%; Score 27; DB 4; Length 988;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATSSRAT 7
Db      626 ATSDRAT 632

Search completed: April 21, 2004, 17:40:05
Job time : 9.42029 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48 ; Search time 4.56522 Seconds

(without alignments)
102.653 Million cell updates/sec

Title: SEQ6

Perfect score: 51

Sequence: 1 QYGSPPCS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	76.5	109	1 KV3G HUMAN	P04206 homo sapien
2	39	76.5	695	1 DVL1 MOUSE	P51141 mus musculus
3	39	76.5	695	1 DVL1 RAT	Q9WV69 rattus norv
4	39	76.5	1235	1 IRS1_MOUSE	P35569 mus musculus
5	39	76.5	1235	1 IRS1_RAT	P35570 rattus norv
6	39	76.5	1242	1 IRS1_HUMAN	P35568 homo sapien
7	39	76.5	4543	1 LRPI_CHICK	P98157 gallus gall
8	38	74.5	108	1 KV3B_HUMAN	P01619 homo sapien
9	38	74.5	109	1 KV3A_HUMAN	P01620 homo sapien
10	38	74.5	109	1 KV3D_HUMAN	P01622 homo sapien
11	38	74.5	129	1 KV3M_HUMAN	P18136 homo sapien
12	35	68.6	100	1 SI07_HUMAN	P31151 homo sapien
13	35	68.6	100	1 SI15_HUMAN	Q86995 homo sapien
14	35	68.6	129	1 KV3L_HUMAN	P18135 homo sapien
15	35	68.6	595	1 2440_HUMAN	Q81Y18 homo sapien
16	35	68.6	899	1 2CH2_HUMAN	Q9C0B9 homo sapien
17	34	66.7	214	1 ENH2_CHLPN	Q92962 chlamydia p
18	34	66.7	276	1 MYO1_ONCMY	Q91205 oncorhynch
19	34	66.7	410	1 TDG_HUMAN	Q13569 homo sapien
20	34	66.7	514	1 PHLD MYCTU	Q3XB13 mycobacteri
21	34	66.7	517	1 PHLC MYCTU	P95245 mycobacteri
22	34	66.7	585	1 TAI2_HUMAN	Q8WY33 homo sapien
23	34	66.7	722	1 DLL1_MOUSE	Q61483 mus musculus
24	34	66.7	843	1 CO7_HUMAN	P10643 homo sapien
25	34	66.7	901	1 RAC3_HUMAN	Q08043 homo sapien
26	34	66.7	1129	1 AKI1_RAT	Q62924 rattus norv
27	34	66.7	1178	1 TSP2_CHICK	P35440 gallus gall
28	33	64.7	140	1 CO8B_RAT	P55314 rattus norv
29	33	64.7	224	1 T257_STRAU	P14506 staphylococ
30	33	64.7	224	1 T431_STAM	P19380 staphylococ
31	33	64.7	271	1 PD5_DROME	P32029 drosophila
32	33	64.7	298	1 SVGA_HELPJ	Q9ZKPI helicobacte
33	33	64.7	486	1 ENV_HTLV2	P03383 human t-cel

34 33 64.7 543 1 CHK2_HUMAN
35 33 64.7 591 1 CO8B_HUMAN
36 33 64.7 598 1 NR42_HUMAN
37 33 64.7 598 1 NR42_MOUSE
38 33 64.7 598 1 NR42_RAT
39 33 64.7 503 1 LCB2_SCHPO
40 33 64.7 710 1 PAL2_ORISA
41 33 64.7 716 1 BAC2_MOUSE
42 33 64.7 841 1 BAC2_HUMAN
43 33 64.7 843 1 CO7_FIG
44 33 64.7 902 1 SYGI_YEAST
45 33 64.7 1075 1 NRC3_MOUSE

O96017 homo sapien
P07358 homo sapien
P43354 homo sapien
Q06219 mus musculus
Q07917 rattus norv
Q09325 schizosacch
P53443 oryza sativ
P97303 mus musculus
Q9BY99 homo sapien
Q9TUG3 sus scrofa
P40528 saccharomyc
P97305 mus musculus

ALIGNMENTS

RESULT 1

KV3G_HUMAN STANDARD; PRT; 109 AA.

AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with anti-peptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR; A01893; K3HUGO.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93598B6 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 109;

Best Local Similarity 88.9%; Pred. No. 0.95;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYGSPPCS 9

Db 90 QYGSPPCS 98

RESULT 2

DVL1_MOUSE STANDARD; PRT; 695 AA.

ID DVL1_MOUSE
AC P51141; Q60868;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE (DSH homolog 1).
GN DVL1 OR DVL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=95046919; PubMed=7958461;
RA Sussman D.J., Klingensmith J., Salinas P., Adams P.S., Nusse R.,
RA Perrimon N.;
RT "Isolation and characterization of a mouse homolog of the Drosophila
RT segment polarity gene dishevelled.";
RL Dev. Biol. 166:73-86(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96232916; PubMed=9132266;
RA Lijam N., Sussman D.J.;
RT "Organization and promoter analysis of the mouse dishevelled-1 gene.";
RL Genome Res. 5:116-124(1995).
RN [3]
RP KNOCK-OUT.
RX MEDLINE=97442352; PubMed=9298901;
RA Lijam N., Paylor R., McDonald M.P., Crawley J.N., Deng C.-X.,
RA Herrup K., Stevens K.E., Maccaferri G., McBain C.J., Sussman D.J.,
RA Wynshaw-Boris A.;
RT "Social interaction and sensorimotor gating abnormalities in mice
RT lacking Dvl1.";
RL Cell 90:895-905(1997).
CC -!- FUNCTION: May play a role in the signal transduction pathway
CC mediated by multiple wnt genes. Dvl1 deficient mice display
CC abnormalities in social behaviors and sensorimotor gating.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: High levels are seen in the brain, testis and
CC kidney, lower levels in the ovary, breast, muscle, liver and small
CC intestine, and very low levels are seen in the spleen and thymus.
CC A moderate level expression is seen in the heart.
CC -!- DEVELOPMENTAL STAGE: Is expressed throughout the embryonic central
CC nervous system from presomite stages and in neuron-rich areas of
CC the brain throughout postnatal development, as well as in many
CC other tissues.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DRH domain.
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DIX domain.
CC -----
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CC -----
CC EMBL; U10115; AA82175.1; -;
CC EMBL; U28138; AA74049.1; -;
CC FDB; 1F5H; 31-DEC-02.
CC MGD; MGI:94941; Dvl1.
CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR008339; Dishevel.
CC InterPro; IPR003351; Dishevelled.
CC InterPro; IPR008340; Dishevelled_1.
CC InterPro; IPR001158; DIX.
CC InterPro; IPR001478; PDZ.
CC Pfam; PF00610; DEP; 1.
CC Pfam; PF02377; Dishevelled; 1.
CC Pfam; PF00778; DIX; 1.
CC Pfam; PF00595; PDZ; 1.
CC PRINTS; PR01760; DISHEVELLED.
CC PRINTS; PR01761; DISHEVELLED1.
CC PRODOM; PD003639; DIX; 1.
CC SMART; SM00021; DAX; 1.
CC SMART; SM00049; DEP; 1.
CC SMART; SM00228; PDZ; 1.

DR PROSITE; PS50186; DEP; 1.
DR PROSITE; PS50841; DIX; 1.
DR PROSITE; PS50106; PDZ; 1.
KW Wnt signaling pathway; Developmental protein; 3D-structure.
FT DOMAIN 1 85 DIX.
FT DOMAIN 251 323 PDZ.
FT DOMAIN 425 499 DEP.
FT DOMAIN 390 393 POLY-SER.
FT CONFLICT 122 125 MISSING (IN REF. 2).
FT CONFLICT 211 211 T -> N (IN REF. 2).
SQ SEQUENCE 695 AA; 75350 MW; A9FA449F95CF75F2 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 695;
Best Local Similarity 75.0%; Pred. No. 6.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYGSPPCS 9
DB 376 RYGTSPCS 383

RESULT 3
ID DVL1_RAT STANDARD; PRT; 695 AA.
AC Q9WVB9; O9QUG5; Q9WVB8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE (DSH homolog 1).
GN DVL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar Kyoto;
RX MEDLINE=21254118; PubMed=11354832;
RA de Lange R.P.J., Burr K., Clark J.S., Negrin C.D., Brosnan M.J.,
RA St Clair D.M., Dominiczak A.F., Shaw D.J.;
RT "Mapping and sequencing rat dishevelled-1: a candidate gene for
RT cerebral ischaemic insult in a rat model of stroke.";
RL Neurogenetics 3:99-106(2001).
CC -!- FUNCTION: May play a role in the signal transduction pathway
CC mediated by multiple Wnt genes.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DRH domain.
CC -!- SIMILARITY: Contains 1 DIX domain.
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CC -----
CC EMBL; AF143545; AAD33896.2; -;
CC EMBL; AF143545; AAD33897.2; -;
CC EMBL; AF143548; AAD41492.2; -;
CC EMBL; AF143547; AAD41492.2; JOINED.
CC EMBL; AF143550; AAD41493.1; -;
CC EMBL; AF143549; AAD41493.1; JOINED.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR008339; Dishevel.
CC InterPro; IPR003351; Dishevelled.
CC InterPro; IPR008340; Dishevelled_1.
CC InterPro; IPR001158; DIX.
CC InterPro; IPR001478; PDZ.
CC Pfam; PF00610; DEP; 1.

RA Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.;
 RT "Pleiotropic insulin signals are engaged by multisite phosphorylation
 of IRS-1";
 RL Mol. Cell. Biol. 13:7418-7428(1993).
 RN [3]
 RP PHOSPHORYLATION SITES
 RX MEDLINE=93352637; PubMed=8349691;
 RA Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
 RA Sacks D.B.;
 RT "Phosphorylation of the insulin receptor substrate IRS-1 by casein
 kinase II";
 RL J. Biol. Chem. 268:18157-18166(1993).
 CC -!- FUNCTION: May mediate the control of various cellular processes by
 CC insulin. When phosphorylated by the insulin receptor binds
 CC specifically to various cellular proteins containing SH2 domains
 CC such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
 CC -!- SIMILARITY: Contains 1 PH domain.
 CC -!- SIMILARITY: Contains 1 PTB domain.
 CC -----
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 CC -----
 CC EMBL; X58375; CAA41264.1; --
 DR HSP; S16948; S16948.
 DR HSP; P35568; IRS.
 DR InterPro; IPR002404; Insln_receptorSl.
 DR InterPro; IPR001849; PH.
 DR Pfam; PF02174; IRS; 1.
 DR Pfam; PF00169; PH; 1.
 DR PRINTS; PR00628; INSULNRSI.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00310; PTB; 1.
 DR PROSITE; PSS0003; PH_DOMAIN; 1.
 KW Phosphorylation.
 FT DOMAIN 12 115 PH.
 FT DOMAIN 152 262 PTB.
 FT DOMAIN 872 881 POLY-GLN.
 FT DOMAIN 1196 1200 POLY-PRO.
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CK2).
 FT MOD_RES 460 460 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 502 502 PHOSPHORYLATION (BY CK2).
 FT MOD_RES 608 608 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 628 628 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 895 895 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 939 939 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 987 987 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 1172 1172 PHOSPHORYLATION (BY INSR).
 FT MOD_RES 1222 1222 PHOSPHORYLATION (BY INSR).
 SQ SEQUENCE 1235 AA; 131178 MW; A274BC7540CA85C5 CRC64;
 Query Match 76.5%; Score 39; DB 1; Length 1235;
 Best Local Similarity 85.7%; Pred.No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QYSSPC 8
 Db 425 EYSSPC 431
 RESULT 6
 ID IRS1_HUMAN STANDARD; PRT; 1242 AA.
 AC P35568;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Insulin receptor substrate-1 (IRS-1).
 GN IRS1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=93292739; PubMed=8513971;
 RA Araki E., Sun X.J., Haag B.L. III, Chuang L.M., Zhang Y.,
 RA Yang-Feng T.L., White M.F., Kahn C.R.;
 RT "Human skeletal muscle insulin receptor substrate-1. Characterization
 of the cDNA, gene, and chromosomal localization.";
 RL Diabetes 42:1041-1054(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92181456; PubMed=1311924;
 RA Nishiyama M., Wands J.R.;
 RT "Cloning and increased expression of an insulin receptor substrate-1
 like gene in human hepatocellular carcinoma.";
 RL Biochem. Biophys. Res. Commun. 183:280-285(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP VARIANTS PRO-512 AND ARG-971.
 RX MEDLINE=93390176; PubMed=8104271;
 RA Almind K., Bjoerbaek C., Vestergaard H., Hansen T., Schwald S.,
 RA Pedersen O.;
 RT "Aminoacid polymorphisms of insulin receptor substrate-1 in
 non-insulin-dependent diabetes mellitus.";
 RL Lancet 342:828-832(1993).
 RN [5]
 RP VARIANT NIDDM GLY-723 DEL.
 RX MEDLINE=96303710; PubMed=8723689;
 RA Esposito D.L., Mammarella S., Ranieri A., della Loggia F., Capani F.,
 RA Consoli A., Mariani-Costantini R., Caramia F.G., Cama A., Battista P.;
 RT "Deletion of Gly723 in the insulin receptor substrate-1 of a patient
 with noninsulin-dependent diabetes mellitus.";
 RL Hum. Mutat. 7:364-366(1996).
 RN [6]
 RP VARIANTS NIDDM TYR-1043 AND TYR-1095.
 RA Mammarella S., Creati B., Esposito D.L., Arcuri P., della Loggia F.,
 RA Capani F., Mariani-Costantini R., Caramia F.G., Battista P., Cama A.;
 RT "Novel allele of the insulin receptor substrate-1 bearing two
 non-conservative amino acid substitutions in a patient with
 noninsulin-dependent diabetes mellitus.";
 RL Hum. Mutat. 11:411-411(1998).
 RN [7]
 RP STRUCTURE BY NMR OF 157-267.
 RX MEDLINE=96185451; PubMed=8599766;
 RA Zhou M.-M., Huang B., Olejniczak B.T., Meadows R.P., Shuker S.B.,
 RA Miyazaki M., Trueb T., Shoelson S.E., Feick S.W.;

RT "Structural basis for IL-4 receptor phosphopeptide recognition by the
 RL Ins-1 PTB domain.";
 CC Nat. Struct. Biol. 3:388-393(1996).
 CC !- FUNCTION: May mediate the control of various cellular processes by
 CC insulin. When phosphorylated by the insulin receptor binds
 CC specifically to various cellular proteins containing SH2
 CC domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
 CC !- DISEASE: POLYMORPHISMS IN IRS1 MAY BE INVOLVED IN THE ETIOLOGY OF
 CC A SUBSET OF LATE-ONSET NON-INSULIN-DEPENDENT DIABETES MELLITUS
 CC (NIDDM).
 CC !- SIMILARITY: Contains 1 PH domain.
 CC !- SIMILARITY: Contains 1 PTB domain.
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 CC EMBL; S95963; AAB21608.1; -;
 CC EMBL; S62539; AAB27175.1; -;
 CC EMBL; BC053895; AAH53895.1; -;
 CC PIR; I53160; JS0670.
 CC PDB; 1JRS; 15-MAY-97.
 CC PDB; 1K3A; 05-DEC-01.
 CC PDB; 1QQG; 10-NOV-99.
 CC Genew; HGNC:6125; IRS1.
 CC MIM; 147545; -;
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0005515; R:protein binding; IPI.
 CC GO; GO:0004871; F:signal transducer activity; TAS.
 CC GO; GO:0005065; F:transmembrane receptor protein tyrosine kin. . .; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR002404; Insln_receptorS1.
 CC InterPro; IPR001849; PH.
 CC Pfam; PF02174; IRS; 1.
 CC Pfam; PF00169; PH; 1.
 CC PRINTS; PR00628; INSLINRS1.
 CC SMART; SM00233; PH; 1.
 CC SMART; SM00310; PTB; 1.
 CC PROSITE; PS00003; PH_DOMAIN; 1.
 CC Phosphorylation; Polymorphism; Diabetes mellitus; Disease mutation;
 KW 3D-structure.
 FT DOMAIN 12 115 PH.
 FT DOMAIN 157 267 PTB.
 FT DOMAIN 128 134 POLY-GLY.
 FT DOMAIN 391 398 POLY-SER.
 FT DOMAIN 680 686 POLY-SER.
 FT DOMAIN 807 815 POLY-SER.
 FT DOMAIN 877 882 POLY-GLN.
 FT DOMAIN 1035 1038 POLY-SER.
 FT DOMAIN 1126 1130 POLY-GLY.
 FT DOMAIN 1131 1135 POLY-SER.
 FT DOMAIN 1197 1207 POLY-PRO.
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CK2)
 FT MOD_RES 465 465 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 612 612 PHOSPHORYLATION (BY INSR)
 FT MOD_RES 632 632 PHOSPHORYLATION (BY INSR)
 FT MOD_RES 896 896 PHOSPHORYLATION (BY INSR)
 FT MOD_RES 941 941 PHOSPHORYLATION (BY INSR)
 FT MOD_RES 989 989 PHOSPHORYLATION (BY INSR)
 FT MOD_RES 1179 1179 PHOSPHORYLATION (BY INSR)
 FT MOD_RES 1229 1229 PHOSPHORYLATION (BY INSR)

FT VARIANT 158 158 (BY SIMILARITY).
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 FT FT M -> T (in dbSNP:1801118).
 FT FT /FTId=VAR 014854.
 FT FT A -> P (in dbSNP:1801276).
 FT FT /FTId=VAR 005299.
 FT FT MISSING (IN NIDDM).
 FT FT /FTId=VAR 005301.
 FT FT S -> F (in dbSNP:1801120).
 FT FT /FTId=VAR 014855.
 FT FT S -> G (in dbSNP:1801277).
 FT FT /FTId=VAR 014856.
 FT FT G -> R (in dbSNP:1801278).
 FT FT /FTId=VAR 005300.
 FT FT S -> Y (IN NIDDM).
 FT FT /FTId=VAR 005302.
 FT FT C -> Y (IN NIDDM).
 FT FT /FTId=VAR 005303.
 FT FT G -> GG (IN REF. 2).
 FT FT S -> R (IN REF. 2).
 FT FT P -> R (IN REF. 2).
 SQ SEQUENCE 1242 AA; 131590 MW; 3C0EFD9E32B3E64A CRC64;
 Query Match 76.5%; Score 39; DB 1; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QYGSPPC 8
 Db 430 EYGSPPC 436
 :|||||
 ID_LRPI_CHICK STANDARD; PRT; 4543 AA.
 AC P98157;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Low-density lipoprotein receptor-related protein 1 precursor (LRP)
 DE (Alpha-2-macroglobulin receptor) (A2MR).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OK NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=white leghorn; TISSUE=Liver, and Ovary;
 RX MEDLINE=9410312; PubMed=7506255;
 RA Nimpf J., Stifani S., Bilous P.T., Schneider W.J.;
 RT "The somatic cell-specific low density lipoprotein receptor-related
 RT protein of the chicken. Close kinship to mammalian low density
 RT lipoprotein receptor gene family members.";
 RL J. Biol. Chem. 269:212-219 (1994).

CC -!- FUNCTION: Involved in the plasma clearance of chylomicron remnants
CC and activated alpha 2-macroglobulin, as well as the local
CC metabolism of complexes between plasminogen activators and their
CC endogenous inhibitors. Binds vitellogenin, calcium and alpha 2-
CC macroglobulin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P98157-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P98157-2; Sequence=VSP_004312;
CC -!- TISSUE SPECIFICITY: Somatic.
CC -!- PTM: Cleaved into a 85 kDa membrane-spanning subunit (LRP-85) and
CC a 515 kDa large extracellular domain (LRP-515) that remains non-
CC covalently associated.
CC -!- SIMILARITY: Contains 22 EGF-like domains.
CC -!- SIMILARITY: Contains 31 LDL-receptor class A domains.
CC -----
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CC EMBL; X74904; CAA52870.1; -;
CC PIR; A53102; A53102.
CC PDB; 1LPX; 29-DEC-99.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR002172; LDL_receptor_A.
CC InterPro; IPR000033; ldl_receptor_rep.
CC Pfam; PF00008; EGF_14.
CC Pfam; PF00057; ldl_recept_a; 31.
CC Pfam; PF00058; ldl_recept_b; 33.
CC PRINTS; PR00261; LDLRECEPTOR.
CC SMART; SM00179; EGF_CA; 3.
CC SMART; SM00192; LDLra; 31.
CC SMART; SM00135; LY; 34.
CC PROSITE; PS00010; ASX_HYDROXYL; 3.
CC PROSITE; PS00022; EGF_1; 5.
CC PROSITE; PS00186; EGF_2; 7.
CC PROSITE; PS00026; EGF_3; 8.
CC PROSITE; PS01187; EGF_CA; 2.
CC PROSITE; PS01209; LDLRA_1; 27.
CC PROSITE; PS50068; LDLRA_2; 31.
CC Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein; Signal;
CC Calcium-binding; EGF-like domain; Coated pits; Alternative splicing;
CC 3D-structure.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 4543 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
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CC TRANSMEM 4420 4443 POTENTIAL.
CC DOMAIN 4444 4543 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 27 68 LDL-RECEPTOR CLASS A 1.
CC DOMAIN 72 112 LDL-RECEPTOR CLASS A 2.
CC DOMAIN 113 151 EGF-LIKE 1.
CC DOMAIN 152 191 EGF-LIKE 2.
CC DOMAIN 191 222 EGF-LIKE 3.
CC DOMAIN 801 841 EGF-LIKE 4.
CC DOMAIN 850 890 LDL-RECEPTOR CLASS A 3.
CC DOMAIN 891 931 LDL-RECEPTOR CLASS A 4.
CC DOMAIN 932 971 LDL-RECEPTOR CLASS A 5.
CC DOMAIN 972 1011 LDL-RECEPTOR CLASS A 6.
CC DOMAIN 1011 1051 LDL-RECEPTOR CLASS A 7.
CC DOMAIN 1058 1097 LDL-RECEPTOR CLASS A 8.
CC DOMAIN 1100 1140 LDL-RECEPTOR CLASS A 9.
CC DOMAIN 1141 1180 LDL-RECEPTOR CLASS A 10.
CC DOMAIN 1181 1220 EGF-LIKE 5.

DOMAIN 1221 1260 EGF-LIKE 6.
DOMAIN 1534 1577 EGF-LIKE 7.
DOMAIN 1842 1883 EGF-LIKE 8.
DOMAIN 2151 2191 EGF-LIKE 9.
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FT DISULFID 1032 1049 BY SIMILARITY.
FT DISULFID 1060 1073 BY SIMILARITY.
FT DISULFID 1067 1086 BY SIMILARITY.
FT DISULFID 1080 1095 BY SIMILARITY.
FT DISULFID 1102 1116 BY SIMILARITY.
FT DISULFID 1110 1129 BY SIMILARITY.
FT DISULFID 1123 1138 BY SIMILARITY.
FT DISULFID 1143 1157 BY SIMILARITY.
FT DISULFID 1150 1170 BY SIMILARITY.
FT DISULFID 1164 1180 BY SIMILARITY.
FT DISULFID 1183 1194 BY SIMILARITY.
FT DISULFID 1190 1204 BY SIMILARITY.
FT DISULFID 1206 1219 BY SIMILARITY.
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FT DISULFID 1231 1244 BY SIMILARITY.
FT DISULFID 1246 1259 BY SIMILARITY.
FT DISULFID 1538 1551 BY SIMILARITY.
FT DISULFID 1547 1561 BY SIMILARITY.
FT DISULFID 1563 1576 BY SIMILARITY.
FT DISULFID 1846 1857 BY SIMILARITY.
FT DISULFID 1853 1867 BY SIMILARITY.
FT DISULFID 1869 1882 BY SIMILARITY.
FT DISULFID 2155 2166 BY SIMILARITY.
FT DISULFID 2162 2176 BY SIMILARITY.
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FT DISULFID 2499 2511 BY SIMILARITY.
FT DISULFID 2518 2531 BY SIMILARITY.
FT DISULFID 2526 2544 BY SIMILARITY.
FT DISULFID 2538 2555 BY SIMILARITY.
FT DISULFID 2560 2572 BY SIMILARITY.
FT DISULFID 2567 2585 BY SIMILARITY.

Query Match 76.5%; Score 39; DB 1; Length 4543;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOYGSPPCS 9
DB 1839 QOAGSNPCS 1847

RESULT 8
KV3A_HUMAN
ID KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6."
RL FEBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01891; K3HUB6.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 74.5%; Score 38; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSPP 7
DB 90 QOYGSPP 96

RESULT 9
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W.; Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
Group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSPP 7
DB 90 QOYGSPP 96

RESULT 10
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L.; Barnikol H.U.; Watanabe S.; Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal

immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR, A01895; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058DCD7749BC CRC64;
 Query Match 74.5%; Score 38; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. NO. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQYGSSP 7
 DB 90 QQYGSSP 96
 RESULT 11
 KV3M HUMAN
 ID KV3M HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
 RT J. Exp. Med. 167:840-852(1988).
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
 CC PIR; P18021; K3HUT1.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 103 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.

FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;
 Query Match 74.5%; Score 38; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. NO. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQYGSSP 7
 DB 110 QQYGSSP 116
 RESULT 12
 S107 HUMAN
 ID S107 HUMAN STANDARD; PRT; 100 AA.
 AC P31151; Q9HUE2;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE S100 calcium-binding protein A7 (Psoriasis).
 GN S100A7 OR PSORI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Keratinocytes;
 RX MEDLINE=92043866; PubMed=1940442;
 RA Madsen P., Rasmussen H.H., Leffers H., Honore B., Dejgaard K., Olsen E., Kii J., Walbum E., Andersen A.H., Basse B., Lauridsen J.B., Ratz G.P., Celis A., Vandeckerckhove J., Celis J.E.;
 RT "Molecular cloning, occurrence, and expression of a novel partially secreted protein 'psoriasis' that is highly up-regulated in psoriatic skin.";
 RT J. Invest. Dermatol. 97:701-712(1991).
 RN [2]
 RP SEQUENCE, AND ACETYLATION.
 RX TISSUE=Psoriatic skin;
 RX MEDLINE=96095666; PubMed=8526920;
 RA Burgisser D.M., Siegenthaler G., Kuster T., Hellman U., Hunziker P., Birchler N., Heizmann C.W.;
 RT "Amino acid sequence analysis of human S100A7 (psoriasis) by tandem mass spectrometry.";
 RT Biochem. Biophys. Res. Commun. 217:257-263(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Skin;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-88 FROM N.A.
 RA Glaeser R., Harder J., Christophers E., Schroeder J.M.;

RT "Genomic organization of human psoriasin (S100A7) gene.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 8-18; 37-47; 49-60; 68-86 AND 88-100.
RC TISSUE=Keratinocytes;
RA MEDLINE=93162043; PubMed=1286667;
RX Rasmussen H.H., van Damme J., Puyte M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RL protein database of normal human epidermal keratinocytes.";
RN Electrophoresis 13:960-969(1992).
[6]
RN TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RP MEDLINE=96212542; PubMed=8618345;
RX Celis J.E., Rasmussen H.H., Vorum H., Madsen P., Honore B., Wolf H.,
RA Orntoft T.F.;
RT "Bladder squamous cell carcinomas express psoriasin and externalize it
RL to the urine.";
RN J. Urol. 155:2105-2112(1996).
[7]
RN X-RAY CRYSTALLOGRAPHY (1.05 ANGSTROMS).
RP MEDLINE=98230746; PubMed=9562557;
RX Brodersen D.E., Rzerodt M., Madsen P., Celis J.E., Thøgersen H.C.,
RA Nyborg J., Kjeldgaard M.;
RT "EF-hands at atomic resolution: the structure of human psoriasin
RL (S100A7) solved by MAD phasing.";
RN Structure 6:477-489(1998).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RP MEDLINE=99152356; PubMed=10026247;
RX Brodersen D.E., Nyborg J., Kjeldgaard M.;
RA "Zinc-binding site of an S100 protein revealed. Two crystal
RT structures of Ca2+-bound human psoriasin (S100A7) in the Zn2+-loaded
RL and Zn2+-free states.";
RN Biochemistry 38:1695-1704(1999).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Also secreted by a non-
CC classical secretory pathway.
CC -!- TISSUE SPECIFICITY: Fetal ear, skin, and tongue and human cell
CC lines. Highly up-regulated in psoriatic epidermis. Also highly
CC expressed in the urine of bladder squamous cell carcinoma (SCC)
CC bearing patients.
CC -!- MASS SPECTROMETRY: MW=11365; MW ERR=0.7; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
CC
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CC
CC EMBL; M86757; AAA60210.1; -;
DR EMBL; BC034687; AAH34687.1; -;
DR EMBL; AJ012825; CAC20409.1; -;
DR PIR; A54327; A54327.
DR PIR; 1PSR; 13-JAN-99.
DR PDB; 2PSR; 15-JUN-99.
DR PDB; 3PSR; 15-JUN-99.
DR Aarhus/Ghent-2DPAGE; 3002; IEF.
DR Genew; HGNC:10497; S100A7.
DR MTM; 600353; -;
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0008544; P:epidermal differentiation; TAS.
DR InterPro; IPR001751; CaBP S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP S100; 1.
DR PROSITE; PS00018; EF HAND; 1.
DR PROSITE; PS00303; S100 CBP; 1.
CC Calcium-binding; Zinc; Metal-binding; Acetylation; 3D-structure.

FT INIT MET 0 0
FT MOD RES 1 1
FT CA BIND 62 73
FT DISULFID 46 95
FT METAL 17 17
FT METAL 24 24
FT METAL 86 86
FT METAL 90 90
FT HELIX 4 18
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FT TURN 22 23
FT STRAND 26 26
FT HELIX 28 38
FT TURN 40 48
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FT TURN 63 64
FT STRAND 69 69
FT HELIX 71 88
FT TURN 89 91
SQ SEQUENCE 100 AA; 11326 MW; 0E361FD5DEA9DCE8 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 100;
Best Local Similarity 55.6%; Pred. No. 5.2;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QYQSSPCS 9
Db 88 QSHGAPCS 96

RESULT 13
S115_HUMAN
ID S115_HUMAN STANDARD; PRT; 100 AA.
AC Q86SGS;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE S100 calcium-binding protein A15.
GN S100A15
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermis;
RX MEDLINE=22881852; PubMed=12923069;
RA Wolf R., Mirzomahmadsadeh A., Waiz M., Lysa B., Tartler U., Remus R.,
RA Hengge U., Michel G., Ruzicka T.;
RT "Molecular cloning and characterization of alternatively spliced mRNA
RT isoforms from psoriatic skin encoding a novel member of the S100
RT family";
RL FASEB J. 17:1969-1971(2003).
CC -!- FUNCTION: May be involved in epidermal differentiation and
CC inflammation and might therefore be important for the pathogenesis
CC of psoriasis and other diseases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: Overexpressed in psoriasis.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
CC
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CC or send an email to license@isb-sib.ch.
CC
CC EMBL; AY189117; AAO400032.1; -;

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DR EMBL; AY189118; AAC040033.1; -
DR EMBL; AY189119; AAC040034.1; -
DR Genbank; HGNC:21657; S100A15.
DR InterPro; IPR001751; CAPP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CAPP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CAPP; 1.
KW Calcium-binding; Zinc; Metal-binding; Acetylation.
FT INIT MET 0
FT MOD_RES 1
FT CA_BIND 62 73
FT METAL 17 17
FT METAL 86 86
FT METAL 90 90
FT METAL 90 90
SQ SEQUENCE 100 AA; 11174 MW; AFE23C8821B507AB CRC64;
Query Match 68.6%; Score 35; DB 1; Length 100;
Best Local Similarity 55.6%; Pred. No. 5.2; Mismatches 3; Indels 1; Gaps 0;
Matches 5; Conservative 3;

QY 1 QYQGSPPCS 9
Db 88 QSHGAPCS 96

RESULT 14
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
CC PIR; P18022; K3HUHA.
CC HSP; P80362; IWL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129
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SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
Query Match 68.6%; Score 35; DB 1; Length 129;
Best Local Similarity 85.7%; Pred. No. 6.8; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;

QY 1 QYQGSPP 7
Db 110 QYQGTSP 116

RESULT 15
Z440_HUMAN STANDARD; PRT; 595 AA.
ID Z440_HUMAN
AC Q8Y1F8; Q8N1R9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 440.
GN ZNF440.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX TISSUE=Tongue;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuna M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Naganari K., Masuho Y., Negai K.,
RA Isogai T.;
RT "NED0 human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RX TISSUE=Uterus;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Trinchman J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in transcriptional regulation.
CC -!- SUBCELLULAR LOCATION: Nuclear (potential).
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
CC -!- SIMILARITY: Contains 1 KRAB domain.
CC -!- SIMILARITY: Contains 12 C2H2-type zinc fingers.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch)

DR EMBL; BC035760; AAH35760.1; -;
DR EMBL; AK095252; BAC04510.1; -;
DR Genew; HGNC:20874; ZNF440.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1; _C2H2.
DR Pfam; PF00096; zf-C2H2; 11.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 11.
DR PROSITE; PS00805; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 12.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repeat.
FT DOMAIN 4 86
FT ZN_FING 144 166
FT ZN_FING 172 194
FT ZN_FING 200 222
FT ZN_FING 228 250
FT ZN_FING 256 278
FT ZN_FING 284 306
FT ZN_FING 312 334
FT ZN_FING 340 362
FT ZN_FING 368 390
FT ZN_FING 396 418
FT ZN_FING 424 448
FT ZN_FING 458 480
FT CONFLICT 40 40
FT CONFLICT 569 569
SQ SEQUENCE 595 AA; 69105 MW; 7DCDFB698E40661 CRC64;
C2H2-TYPE 1 (DEGENERATE).
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
C2H2-TYPE 5 (DEGENERATE).
C2H2-TYPE 6.
C2H2-TYPE 7.
C2H2-TYPE 8.
C2H2-TYPE 9.
C2H2-TYPE 10.
C2H2-TYPE 11.
C2H2-TYPE 12.
L -> M (IN REF. 1).
S -> N (IN REF. 1).

Query Match 68.6%; Score 35; DB 1; Length 595;
Best Local Similarity 62.5%; Pred. NO. 33;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QYGSPPC 8
DB 137 QYGPKEC 144

Search completed: April 21, 2004, 17:34:02
Job time : 5.56522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:26:23 ; Search time 24 Seconds
(without alignments)
118.319 Million cell updates/sec

Title: SEQ6

Perfect score: 51

Sequence: 1 qqyspspe 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*

1: sp_archea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_prodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	412	Q8NA39	Q8NA39 homo sapien
2	39	76.5	885	Q91615	Q91615 xenopus lae
3	39	76.5	1240	P79773	P79773 gallus gall
4	39	76.5	1251	Q28224	Q28224 cercopithec
5	38	74.5	109	Q9UL78	Q9UL78 homo sapien
6	36	70.6	517	Q7U7H0	Q7U7H0 rhodospirill
7	36	70.6	524	Q9LGG9	Q9LGG9 oryza sativ
8	36	70.6	591	Q8RD12	Q8RD12 thermocoaer
9	35	68.6	151	Q8CB29	Q8CB29 mus musculu
10	35	68.6	174	Q9AFD0	Q9AFD0 rhizobium m
11	35	68.6	174	Q92TG3	Q92TG3 rhizobium m
12	35	68.6	267	Q3PUA5	Q3PUA5 xenopus lae
13	35	68.6	298	Q9NKF6	Q9NKF6 homo sapien
14	35	68.6	347	Q8K340	Q8K340 mus musculu
15	35	68.6	362	Q8COD3	Q8COD3 mus musculu
16	35	68.6	584	Q8BL43	Q8BL43 mus musculu

ALIGNMENTS

RESULT 1

ID	Q8NA39	PRELIMINARY;	PRT;	412 AA.
AC	Q8NA39;			
DC	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein FLJ35870.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TiSSUE=Testis;			
RA	Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,			
RA	Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Chiba Y.,			
RA	Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,			
RA	Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,			
RA	Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,			
RA	Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,			
RA	Wagatsuma M., Takahashi-Fujii A., Ohnima A., Sugiyama A., Kawakami B.,			
RA	Suzuki Y., Sugano S., Nagahari K., Masuno Y., Negai K., Isogai T.;			
RT	"NEDO human cDNA sequencing project.";			
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
EMBL	AK093189; BAC04089.1; ..			
DR	GO; GO:0004871; P:signal transducer activity; IEA.			
DR	GO; GO:0007275; P:development; IEA.			
DR	GO; GO:0007222; P:frizzled signaling pathway; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	InterPro; IPR000591; DEP.			
DR	InterPro; IPR008339; Dishevelled_1.			
DR	InterPro; IPR001478; PDZ.			
DR	Pfam; PF00610; DEP; 1.			
DR	Pfam; PF00595; PDZ; 1.			
DR	PRINTS; PR01760; DISHEVELLED.			
DR	PRINTS; PR01761; DISHEVELLED.			
DR	SMART; SM00049; DEP; 1.			

17	35	68.6	745	10	Q93XR7	Q93xr7 bruguiera g
18	35	68.6	746	13	Q7ZY80	Q7zy80 xenopus lae
19	35	68.6	1135	10	Q84W49	Q84w49 arabidopsis
20	35	68.6	1192	10	Q9S7T0	Q9s7t0 arabidopsis
21	35	68.6	2870	5	Q950C2	Q950c2 caenorhabdi
22	35	68.6	4823	13	Q93321	Q93321 fugu rubrip
23	34	66.7	138	10	Q8H5N8	Q8h5n8 oryza sativ
24	34	66.7	139	16	Q9ACX8	Q9acx8 streptomyce
25	34	66.7	150	11	Q9QZU5	Q9qzu5 mus musculu
26	34	66.7	235	4	Q96MX9	Q96mx9 homo sapien
27	34	66.7	276	13	Q7ZZN1	Q7zzn1 salmo salar
28	34	66.7	318	8	Q7Y8W0	Q7y8w0 portunus tr
29	34	66.7	347	16	Q8G4A1	Q8g4a1 bifidobacte
30	34	66.7	358	4	Q8NAB9	Q8nab9 homo sapien
31	34	66.7	373	16	P96397	P96397 mycobacteri
32	34	66.7	378	5	Q86JA7	Q86ja7 dictyosteli
33	34	66.7	387	5	Q9GYV5	Q9gyv5 drosophila
34	34	66.7	387	5	Q9W105	Q9w105 drosophila
35	34	66.7	388	16	Q7U2J8	Q7u2j8 mycobacteri
36	34	66.7	393	3	Q13963	Q13963 schizosacch
37	34	66.7	397	16	Q8A529	Q8a529 bacteroides
38	34	66.7	410	4	Q8I2M3	Q8i2m3 homo sapien
39	34	66.7	410	4	Q8IUZ6	Q8iuz6 homo sapien
40	34	66.7	491	11	Q8BH27	Q8bh27 mus musculu
41	34	66.7	512	5	Q8IFW9	Q8ifw9 ciona intes
42	34	66.7	539	10	Q8LNI4	Q8lni4 oryza sativ
43	34	66.7	541	3	Q87ID0	Q87id0 neurospora
44	34	66.7	560	13	Q7T0S1	Q7t0s1 xenopus lae
45	34	66.7	567	12	Q9EMS7	Q9ems7 amaecta moo

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DR PROSITE; P850186; DEP; 1.
DR PROSITE; P850106; PDZ; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 412 AA; 43743 MW; 93C3ABB1BF01C207 CRC64;

Query Match 76.5%; Score 39; DB 4; Length 412;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSSPCS 9
DB 93 RYGTSPCS 100
:|||||

RESULT 2
Q91615 PRELIMINARY; PRT; 885 AA.
ID Q91615
AC Q91615;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Insulin receptor substrate-1-like protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu J.X., Sorisky A., Zhu L., Pawson T.;
RT "Molecular cloning of an Amphibian Insulin Receptor Substrate-1-like
RT cDNA and Involvement of Phosphatidylinositol 3-Kinase in Insulin-
RT Induced Xenopus Oocyte Maturation.";
RL Mol. Cell. Biol. 15:0-0(1995).
DR EMBL; U27842; AAA73572.1; -.
DR HSPB; P35568; IIRS.
DR GO; GO:0005158; F:insulin receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002404; F:insln_receptorS1.
DR Pfam; PF02174; IRS_1.
DR PRINTS; PR00628; INSULINRSI.
DR SMART; SM00310; PTB1; 1.
KW Receptor.
SQ SEQUENCE 885 AA; 96146 MW; 9F1B96C64949CA7D CRC64;

Query Match 76.5%; Score 39; DB 13; Length 885;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSSPC 8
DB 223 EYGSSPC 229
:|||||

RESULT 3
P79773 PRELIMINARY; PRT; 1240 AA.
ID P79773
AC P79773;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Insulin receptor substrate 1.
OS IRS-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Leghorn;
RC MEDLINE=97080546; PubMed=8921891;
RA Taouis M., Taylor S.I., Reitman M.;

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RT  "cloning of the chicken insulin receptor substrate 1 gene."
RL  Gene 178:51-55(1996).
CC  -I- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR  EMBL; U43502; AAC60050.1; -.
DR  PIR; JC5209; JCS209.
DR  KSSP; P35568; 1IRS.
DR  GO; GO:0005158; Finsulin receptor binding; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  InterPro; IPR002404; Insln_receptors1.
DR  InterPro; IPR001849; PH.
DR  Pfam; PF02174; IRS; 1.
DR  Pfam; PF00169; PH; 1.
DR  PRINTS; PR00628; INSULINRS1.
DR  SMART; SM00233; PH; 1.
DR  SMART; SM00310; PTBI; 1.
DR  PROSITE; PS50003; PH_DOMAIN; 1.
KW  Receptor.
SQ  SEQUENCE 1240 AA; 131813 MW; 7FDEB2CEADECA7B6 CRC64;

      Query Match          76.5%; Score 39; DB 13; Length 1240;
      Best Local Similarity 85.7%; Pred.No. 39;
      Matches 6; Conservative 1; Mismatches 0; Indels

QY  2 QYGSPPC 8
DB  428 EYGSPPC 434
      :|||||

RESULT 4
Q28224 PRELIMINARY; PRT; 1251 AA.
AC Q28224;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE IRS-1(COS).
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96067569; PubMed=7488107;
RA Wang L., Hayashi H., Mitani Y., Ishii K., Ohnishi T., Niwa Y., Kido H., Ebina Y.;
RT "Cloning of a cDNA encoding a 190-kDa insulin receptor substrate like protein of simian COS cells."
RL Biochem. Biophys. Res. Commun. 216:321-328(1995).
CC -I- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; D64157; BAAL1026.1; -.
DR KSSP; P35568; 1IRS.
DR GO; GO:0005158; F:insulin receptor binding; IEA.
DR InterPro; IPR002404; Insln_receptors1.
DR InterPro; IPR001849; PH.
DR Pfam; PF02174; IRS; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00628; INSULINRS1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00310; PTBI; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
SQ SEQUENCE 1251 AA; 133054 MW; 92ACAC3B568EB98 CRC64;

      Query Match          76.5%; Score 39; DB 6; Length 1251;
      Best Local Similarity 85.7%; Pred.No. 39;
      Matches 6; Conservative 1; Mismatches 0; Indels

QY  2 QYGSPPC 8
DB  430 EYGSPPC 436
      :|||||

RESULT 5

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ID	Q9UL78	PRELIMINARY;	PRT;	109 AA.
AC	Q9UL78;			
DT	01-WAY-2000 (TREMBLrel. 13, Created)			
DT	01-WAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Myosin-reactive immunoglobulin light chain variable region (fragment).			
OS	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;				
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=98277139; PubMed=9614934;			
RP	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	feetus";			
RL	Clin. Immunol. Immunopathol. 87:184-192 (1998).			
DR	EMBL; AF035036; AAD56272.1; -.			
DR	PIR; A30601; A30601.			
DR	PIR; A30608; A30608.			
DR	PIR; B30601; B30601.			
DR	PIR; B30607; B30607.			
DR	PIR; C30601; C30601.			
DR	PIR; C30607; C30607.			
DR	PIR; C30608; C30608.			
DR	PIR; D30601; D30601.			
DR	PIR; D30607; D30607.			
DR	PIR; D30608; D30608.			
DR	PIR; F30607; F30607.			
DR	PIR; F30608; F30608.			
DR	PIR; G30601; G30601.			
DR	PIR; G30608; G30608.			
DR	PIR; H30607; H30607.			
DR	PIR; I30608; I30608.			
DR	PIR; I30601; I30601.			
DR	PIR; PH0963; PH0963.			
DR	PIR; PH0965; PH0965.			
DR	PIR; S34096; S34096.			
DR	HSSP; P80362; LWIL.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SMC0406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER 1			
FT	NON_TER 109			
FT	NON_TER 109			
SQ	SEQUENCE 109 AA; 11646 MW; 5F67C5C28C7BE197 CRC64;			
Query Match 74.5%; Score 38; DB 4; Length 109;				
Best Local Similarity 100.0%; Pred.No. 5.2;				
Matches 7; Conservative 0; Mismatches 0; Indels 0;				
Qy	1 QYGGSSP 7			
Db	90 QYGGSSP 96			
RESULT 6				
Q7UFH0				
ID	Q7UFH0	PRELIMINARY;	PRT;	517 AA.
AC	Q7UFH0			
DT	01-OUT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Hydrothermal protein.			
GN	R8557;			
OS	Rhodospirillum rubrum.			
OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;			
OC	Planctomycetaceae; Pirellula			
OX	NCBI TaxID=117;			

```

OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RA MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.,
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AF012996; AM23537.1; -.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002772; Glyco_hydro_3C.
DR InterPro; IPR001764; Glyco_hydro_3N.
DR Pfam; PF00933; Glyco_hydro_3; 1.
DR Pfam; PF01915; Glyco_hydro_3_C; 1.
DR PRINTS; PR00133; GLYDRLASE3.
KW Glycosidase; Complete proteome.
SQ SEQUENCE 591 AA; 64817 MW; EBF5A938DEA54101 CRC64;

Query Match 70.6%; Score 36; DB 16; Length 591;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYGSPPCS 9
DB 550 QYGMNPCS 557

RESULT 9
Q8CB29 PRELIMINARY; PRT; 151 AA.
AC Q8CB29;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RA MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK036917; BAC29638.1; -.
KW Hypothetical protein.
SQ SEQUENCE 151 AA; 16328 MW; C54CBC212D283BAF CRC64;

Query Match 68.6%; Score 35; DB 11; Length 151;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGSPPCS 9
DB 58 YGVSPCS 64

RESULT 10
Q9AFD0 PRELIMINARY; PRT; 174 AA.
AC Q9AFD0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Paad.
GN PAAD.

OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M.P.F., Batague L.J., Legares A.;
RA "Putative Sinorhizobium meliloti gene cluster for phenylacetic acid
RT degradation.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350436; AA29442.1; -.
DR InterPro; IPR002744; DUF59.
DR Pfam; PF01883; DUF59; 1.
DR ProDom; PD005595; DUF59; 1.
SQ SEQUENCE 174 AA; 18973 MW; 349FF670182ADF2E CRC64;

Query Match 68.6%; Score 35; DB 2; Length 174;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
DB 149 QFGSTPC 155

RESULT 11
Q92TG3 PRELIMINARY; PRT; 174 AA.
AC Q92TG3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative phenylacetic acid degradation protein.
GN PAAD OR RB1557 OR SMB21637.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21395508; PubMed=11491431;
RA Finan T.M., Weidner S., Wong K., Buhrmaster J., Chain P., Gouzy J.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL803647; CAC49956.1; -.
DR PIR; D86036; D96036.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR002744; DUF59.
DR Pfam; PF01883; DUF59; 1.
DR ProDom; PD005595; DUF59; 1.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 174 AA; 19029 MW; ABE64850182DD83C CRC64;

Query Match 68.6%; Score 35; DB 16; Length 174;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
DB 149 QFGSTPC 155

RESULT 12
Q9PUA5 PRELIMINARY; PRT; 267 AA.
AC Q9PUA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
GN PAAD.

```

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE bZIP transcription factor L-Maf.
 GN MAF.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21152895; PubMed=11231068;
 RA Ishibashi S., Yasuda K.;
 RT "Distinct roles of maf genes during Xenopus lens development.";
 RL Mech. Dev. 101:155-166(2001).
 DR EMBL; AF202059; AAF08317.2; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008917; Euk.transcr_DNA.
 DR InterPro; IPR004827; TF_Maf.
 DR Pfam; PF03131; bZIP_Maf; 1.
 DR SMART; SM00338; BRLZ; 1.
 DR PROSITE; PS0217; BZIP; 1.
 SQ SEQUENCE 267 AA; 29637 MW; 2F48837AD0675232 CRC64;

Query Match 68.6%; Score 35; DB 13; Length 267;
 Best Local Similarity 66.7%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 Db 42 QSLGSPPCS 50

RESULT 13
 Q9NKF6 PRELIMINARY; PRT; 298 AA.
 AC Q9NKF6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ20291.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M.,
 RA Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isegai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK000288; BA91057.1; -.
 DR GO; GO:000288; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; ZNF_C2HC; 1.
 DR PROSITE; PS0158; ZF_CCHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 298 AA; 30699 MW; C2195F66A7E861B CRC64;

Query Match 68.6%; Score 35; DB 4; Length 298;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOYGSPPC 8
 Db 125 QQMGSGPC 132

RESULT 14
 Q8K340 PRELIMINARY; PRT; 347 AA.
 AC Q8K340;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028854; AAH28854.1; -.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro; IPR000159; RA_domain.
 DR PROSITE; PS50200; RA; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 347 AA; 39160 MW; 306E40D38A14B3DE CRC64;

Query Match 68.6%; Score 35; DB 11; Length 347;
 Best Local Similarity 77.8%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 Db 128 QOQFSSPCS 136

RESULT 15
 Q8C0D3 PRELIMINARY; PRT; 362 AA.
 AC Q8C0D3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical serine-rich region/aminocyl-transfer RNA synthetases
 DE class-II containing protein.
 GN 463241JJ06RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=1246851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR EMBL; AK01680; BAC27498.1; -.
 DR MGD; MGI:1925998; 463241JJ06RIK.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro; IPR000159; RA_domain.
 DR PROSITE; PS50200; RA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 362 AA; 40933 MW; 32B1047ACC07B987 CRC64;

Query Match 68.6%; Score 35; DB 11; Length 362;
 Best Local Similarity 77.8%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
 Db 192 QOQFSSPCS 200

Search completed: April 21, 2004, 17:37:23
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:18 ; Search time 36 Seconds
(without alignments)
70.637 Million cell updates/sec

Title: SEQ6

Perfect score: 51

Sequence: 1 qyygssps 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A Geneseq 29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	78.4	87	AAU43833	Propionib
2	40	78.4	87	ABM40352	Propionib
3	39	76.5	412	ADB65321	Human pro
4	39	76.5	695	AAV97560	Mouse Dis
5	39	76.5	695	ABG71359	Mouse dis
6	39	76.5	1155	AAR28047	IRS-1 pro
7	39	76.5	1225	AAO16354	Rat IRSAL
8	39	76.5	1242	AAV13461	Amino aci
9	39	76.5	1242	AAW93972	Human IRS
10	39	76.5	1242	AAAB83921	Amino aci
11	39	76.5	1242	ABB99797	Amino aci
12	39	76.5	1242	ABG72369	Human Ins
13	39	76.5	1242	ABG72372	Human Ins
14	39	76.5	1242	ABG72370	Human Ins
15	39	76.5	1242	ABG72371	Human Ins
16	39	76.5	1242	ABG72368	Human Ins
17	39	76.5	1242	ADA00642	Human IRS
18	39	76.5	1243	AAR67708	Insulin r
19	38	74.5	8	ABP62398	Human imm
20	38	74.5	9	AAW24773	Human imm
21	38	74.5	9	AAW80140	Light cha
22	38	74.5	9	AAV40425	Amino aci
23	38	74.5	9	AAAB67495	Human I19
24	38	74.5	9	ABG78316	Human Fv
25	38	74.5	9	ABP62421	Human imm

26	38	74.5	9	ABP62407	Human imm
27	38	74.5	9	ABP62414	Human imm
28	38	74.5	9	ABP62458	Human imm
29	38	74.5	9	ABP62408	Human imm
30	38	74.5	9	ABP62423	Human imm
31	38	74.5	9	ABP62460	Human imm
32	38	74.5	9	ABP62395	Human imm
33	38	74.5	9	ABP62406	Human imm
34	38	74.5	9	ABP62419	Human imm
35	38	74.5	9	ABP62402	Human imm
36	38	74.5	9	ABP62422	Human imm
37	38	74.5	9	ABP62426	Human imm
38	38	74.5	9	ABP62420	Human imm
39	38	74.5	9	ABP62457	Human imm
40	38	74.5	9	ABP62401	Human imm
41	38	74.5	9	ABP62404	Human imm
42	38	74.5	9	ABP62416	Human imm
43	38	74.5	9	ABP62461	Human imm
44	38	74.5	9	ABP62409	Human imm
45	38	74.5	9	ABP62413	Human imm

ALIGNMENTS

RESULT 1
AAU43833
ID AAU43833 standard; protein; 87 AA.
XX
AC AAU43833;
XX
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #4729.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX N-PSDB; AAS59521.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 5028; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory

polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesizing the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours). The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

Sequence 412 AA;

Query Match 76.5%; Score 39; DB 7; Length 412;
Best Local Similarity 75.0%; Pred. NO. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 9
DB 93 RYGTSPCS 100
:|||||

RESULT 4
AA97560
ID AA97560 standard; protein; 695 AA.

AC AA97560;
DT 05-APR-2001 (first entry)
DE Mouse Dishevelled-1 protein sequence.

KW Mouse; Hedgehog signalling pathway; inhibitor; autoimmune disorder;
KW epithelial cell hyperplasia; fibrosis; inflammation; adenocarcinoma;
KW immune disorder; cancer; thyroiditis; insulin; multiple sclerosis;
KW iridocyclitis; uveitis; orchitis; hepatitis; Addison's disease; asthma;
KW myasthenia gravis; rheumatoid arthritis; lupus erythematosus; emphysema;
KW adult respiratory distress syndrome; chronic bronchitis; atelectasis;
KW silicosis; hypersensitivity pneumonitis; idiopathic pulmonary fibrosis;
KW pneumonia; pleural fibrosis; atherosclerosis; myocardial infarction;
KW gastrointestinal tract disorder; hepatic disease; Alzheimer's disease;
KW Wnt signalling pathway; BMP signalling pathway; sonic hedgehog;
KW Dishevelled-1; Dvl-1.

OS Mus musculus.

XX WO200074706-A1.

PN 14-DEC-2000.

PD 05-JUN-2000; 2000WO-GB002191.

PF 08-JUN-1999; 99GB-00013350.

XX 16-SEP-1999; 99GB-00021953.

XX (LORA-) LORANTIS LTD.

XX Lamb JR, Hoyne GF, Dallman MJ;

XX WPI; 2001-061652/07.

DR N-PSDB; AAA37898.

XX Use of an inhibitor of a Hedgehog signaling pathway in preparation of a
PT medicament for treating epithelial cell hyperplasia, inflammation, cancer
or an immune disorder.

PS Disclosure; Page 71; 78pp; English.

XX This sequence is mouse dishevelled-1 (Dvl-1), and is part of the Hedgehog
CC signalling pathway. The invention relates to the use of an inhibitor of a
CC Hedgehog signalling pathway, or an inhibitor of a target pathway of the
CC Hedgehog signalling pathway, in the preparation of a medicament for
CC treating epithelial cell hyperplasia, fibrosis of tissue, inflammation,
CC cancer (especially adenocarcinoma) or an immune disorder. The immune
CC disorder can be an autoimmune disorder such as thyroiditis, insulinis,
CC multiple sclerosis, iridocyclitis, uveitis, orchitis, hepatitis,
CC Addison's disease, myasthenia gravis, rheumatoid arthritis or lupus
CC erythematosus. Medicament containing the inhibitors is also useful for
CC treating lung or kidney diseases such as adult respiratory distress
CC syndrome, chronic obstructive airway disorders including asthma, disease
CC emphysema and chronic bronchitis, atelectasis, occupational lung disease
CC including silicosis, hypersensitivity diseases of lung such as
CC hypersensitivity pneumonitis, idiopathic interstitial lung diseases such
CC as idiopathic pulmonary fibrosis, pneumonia including interstitial
CC pneumonia, degenerative interstitial pneumonia and acute interstitial
CC pneumonia, and pleural fibrosis. They can also be used in the treatment
CC of inflammation associated with atherosclerosis, e.g. myocardial
CC infarction, diseases of the gastrointestinal tract, hepatic diseases and
CC diseases of the central nervous system e.g. Alzheimer's disease. The
CC Hedgehog signalling pathway is that of Sonic hedgehog, Indian hedgehog or
CC Desert hedgehog, the target pathway of the hedgehog signalling pathway is
CC Wnt or BMP signalling pathway

XX Sequence 695 AA;

Query Match 76.5%; Score 39; DB 4; Length 695;
Best Local Similarity 75.0%; Pred. NO. 2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 9
DB 376 RYGTSPCS 383
:|||||

RESULT 5

ABG71359
ID ABG71359 standard; protein; 695 AA.

XX ABG71359;

XX 23-JAN-2003 (first entry)

DE Mouse dishevelled-1 (Dvl-1) polypeptide.

XX Mouse; Hedgehog signalling pathway; T-cell mediated disease;
KW T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate;
KW ovary; T-cell activation; T-cell proliferation; lymphoma; carcinoma;
KW autoimmune disease; inflammatory disease; proliferative disorder;
KW viral infection; genetic immunodeficiency; neurodegenerative disease;
KW myelodysplastic syndrome; ischaemic injury; toxin-induced disease;
KW wasting disease; dishevelled-1; Dvl-1.

XX Mus musculus.

XX WO200280952-A2.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-GB001666.

XX 09-APR-2001; 2001GB-00008872.

XX 09-APR-2001; 2001GB-00008873.

XX (LORA-) LORANTIS LTD.

XX Lamb JR, Hoyne GF, Dallman MJ, Champion BR;
 XX WPI; 2003-058470/05.
 XX N-PSDB; A8553984.
 XX Use of a modulator of Hedgehog signaling pathways for treating T-cell
 PT mediated disease or infection and diseases associated with increased or
 PT decreased T-cell apoptosis and T-cell proliferation.
 XX
 XX Disclosure; Page 150; 154pp; English.
 XX
 XX The invention relates to use of a modulator of a Hedgehog signalling
 CC pathway or a modulator of a target of the pathway in the preparation of a
 CC medicament for treating T-cell mediated disease or infection or a disease
 CC or disorder associated with increased or decreased T-cell apoptosis and
 CC for modification of (peripheral) T-cell activation or proliferation or T-
 CC cell apoptosis, and for modulation of the Notch signalling pathway in
 CC immune cells. The modulator is useful for treating cancer of the breast,
 CC prostate or ovary, lymphomas and carcinomas, autoimmune diseases such as
 CC systemic lupus erythematosus, multiple sclerosis and diabetes,
 CC inflammatory diseases such as osteoarthritis and Crohn's disease,
 CC proliferative disorders such as atherosclerosis and psoriasis, viral
 CC infections such as AIDS and herpesviruses, genetic immunodeficiencies,
 CC neurodegenerative diseases such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as aplastic anaemia, ischaemic
 CC injuries such as myocardial infarction, toxin-induced diseases such as
 CC cirrhosis and wasting diseases such as cachexia. This sequence represents
 CC the mouse dishevelled-1 (Dvl-1) protein
 XX
 XX Sequence 695 AA;
 Query Match 76.5%; Score 39; DB 6; Length 695;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGS3PCS 9
 Db 376 RYGTSPCS 383
 RESULT 6
 AAR28047
 ID AAR28047 standard; protein; 1155 AA.
 XX
 XX AAR28047;
 XX
 XX 25-MAR-2003 (revised)
 DT 17-MAR-1993 (first entry)
 XX
 XX IRS-1 protein.
 XX
 XX Insulin receptor substrate-1; IRS-1; probe; vector; transform;
 KW IRS-1 metabolism; insulin related disease.
 XX
 XX Rattus rattus.
 OS
 XX WO9213083-A1.
 XX
 XX 06-AUG-1992.
 XX
 XX 17-JAN-1992; 92WO-US000437.
 XX
 XX 18-JAN-1991; 91US-00643982.
 XX
 XX (JOSL-) JOSLIN DIABETES CENT INC.
 XX
 XX Kahn CR, White MF, Rothenberg PL;
 PI WPI; 1992-365881/44.
 XX N-PSDB; AAQ29703.
 XX
 XX Purified nucleic acid encoding Insulin Receptor Substrate - used to

PT prepare IRS-1, for diagnosis and treatment of insulin related diseases
 PT and abnormal cellular proliferation.
 XX
 XX Disclosure; Fig 12; 128pp; English.
 XX
 XX The sequence given is the rat insulin receptor substrate-1 (IRS-1). The
 CC IRS-1 gene was isolated using the probe sequences given in AAQ29701-02.
 CC The IRS-1 sequence can be inserted into a vector and used to transform
 CC cells to produce IRS-1. The level of IRS-1 metabolism can then be studied
 CC and abnormal levels may be seen to be indicative of insulin related
 CC disease. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 XX Sequence 1155 AA;
 Query Match 76.5%; Score 39; DB 2; Length 1155;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGS3PC 8
 Db 385 EYGS3PC 391
 RESULT 7
 AAO16354
 ID AAO16354 standard; protein; 1235 AA.
 XX
 XX AAO16354;
 XX
 XX 03-APR-2003 (first entry)
 DT
 XX Rat IRSAL-related protein.
 XX
 XX Rat; IRSAL; insulin activity modification; saccharide intake;
 KW Gene diagnosis; screening; type II diabetes.
 XX
 XX Rattus sp.
 OS
 XX WO200283730-A1.
 FN
 XX 24-OCT-2002.
 PD
 XX 10-APR-2002; 2002WO-JP003579.
 XX
 XX 10-APR-2001; 2001JP-00111864.
 PR
 XX (TAIS) TAISHO PHARM CO LTD.
 XX
 XX Takahashi S, Hakuno F, Kurihara S;
 PI WPI; 2003-075521/07.
 XX N-PSDB; AAL51458.
 DR
 XX Novel protein IRSAL and encoding gene for modifying insulin physiological
 PT activity and controlling intake of saccharides into cells, applicable in
 PT gene diagnosis and screening e.g. drug candidates for type II diabetes.
 PT
 XX Claim 1; Page 40-48; 58pp; Japanese.
 PS
 XX The invention comprises the amino acid and coding sequence of the IRSAL
 CC protein which functions to modify insulin physiological activity and
 CC control the intake of saccharides into cells. The DNA and protein
 CC sequences of the invention are useful in gene diagnosis and screening
 CC (e.g. drug candidates for type II diabetes). The present amino acid
 CC sequence represents a rat IRSAL-related protein
 XX
 XX Sequence 1235 AA;
 Query Match 76.5%; Score 39; DB 6; Length 1235;
 Best Local Similarity 85.7%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGS3PC 8


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Db      425 EYGSSPC 431
      :|||||
RESULT 8
AAV13461
ID AAV13461 standard; protein; 1242 AA.
XX AC AAV13461;
XX DT 26-JUL-1999 (first entry)
XX DE Amino acid sequence of human IRS-1 protein.
XX KW Phosphotyrosine interaction domain; PI domain; modulator; APP;
XX KW amyloid precursor protein; cytoplasmic domain; Alzheimer's disease;
XX KW neurodegenerative disease; dementia; IRS-1.
XX OS Homo sapiens.
XX PN WO9921995-A1.
XX PD 06-MAY-1999.
XX PF 23-OCT-1998; 98WO-US022523.
XX PR 24-OCT-1997; 97US-00957660.
XX PR 17-APR-1998; 98US-00062085.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Sabo S, Buxbaum J, Greengard P;
XX WPI; 1999-326703/27.
XX Cell line for screening agents that inhibit processing of amyloid
XX precursor protein.
XX Claim 4; Fig 16; 86pp; English.
XX The invention relates to modulators that affect the interaction of a
XX polypeptide defining a PI (phosphotyrosine interaction) domain, or its
XX conserved variants or fragments, with APP (amyloid precursor protein).
XX The polypeptide defining a PI domain binds to the cytoplasmic domain of
XX APP, regulating the secretion of APP fragments. By modulating this
XX interaction, the modulator can inhibit or prevent APP processing and
XX trafficking, and thus progress or onset of Alzheimer's disease. The
XX modulators are used to treat and/or prevent neurodegenerative diseases in
XX mammals, particularly Alzheimer's disease and dementia. Sequences
XX AAV13448-461 represent examples of polypeptides defining a PI domain
XX
SQ Sequence 1242 AA;
Query Match 76.5%; Score 39; DB 2; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSSPC 8
Db 430 EYGSSPC 436
      :|||||
RESULT 9
AAW93972
ID AAW93972 standard; protein; 1242 AA.
XX AC AAW93972;
XX DT 30-JUN-1999 (first entry)
XX DE Human IRS-1 and IRS-2 binding inhibitor protein.
XX DE Insulin receptor substrate; IRS-1; IRS-2; inhibitor; disease; obesity;

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```

KW insulin resistance; 14-3-3 protein; inhibitor; screening; diabetes;
KW diabetic retinopathy; diabetic neuropathy; glucose tolerance;
KW diabetic nephropathy; hyperinsulinaemia; hyperlipemia; arteriosclerosis;
KW hypertension; ischaemic heart disease; ischaemic brain disease;
KW peripheral embolism.
XX OS Homo sapiens.
XX PN WO9916462-A1.
XX PD 08-APR-1999.
XX PF 25-SEP-1998; 98WO-JP004293.
XX PR 29-SEP-1997; 97JP-00263719.
XX PA (DAUC ) DAIICHI PHARM CO LTD.
XX PI Yazaki Y, Asano T, Kubo H, Kanda A;
XX WPI; 1999-254929/21.
XX Treatment of insulin resistance using insulin receptor substrate binding
XX inhibitor.
XX Disclosure; Page 16-22; 30pp; Japanese.
XX This invention describes a method for the treatment of diseases involving
XX insulin resistance using a substance which inhibits the binding of
XX insulin receptor substrate to 14-3-3 protein, identified by screening
XX potential inhibitors for their ability to inhibit this binding. The
XX composition described in the invention for the treatment of diseases
XX involving insulin resistance contains as active component, an inhibitor
XX of the binding of all or part of insulin receptor substrate 1 or 2 (IRS-
XX 1, IRS-2) to all or part of 14-3-3 protein. Disorders involving insulin
XX resistance include diabetes, diabetic retinopathy, diabetic neuropathy,
XX impaired glucose tolerance, diabetic nephropathy, hyperinsulinaemia,
XX hyperlipemia, arteriosclerosis, hypertension, obesity, ischaemic heart
XX disease, ischaemic brain disease and peripheral embolism
XX
SQ Sequence 1242 AA;
Query Match 76.5%; Score 39; DB 2; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSSPC 8
Db 430 EYGSSPC 436
      :|||||
RESULT 10
AAB83921
ID AAB83921 standard; protein; 1242 AA.
XX AC AAB83921;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of a human insulin receptor substrate (IRS).
XX KW Epidermal growth factor-like domain; EGF-like domain; cancer;
XX KW human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour;
XX KW insulin receptor substrate; IRS.
XX OS Homo sapiens.
XX PN WO200135102-A2.
XX PD 17-MAY-2001.
XX PF 08-NOV-2000; 2000WO-US030738.

```

PR 08-NOV-1999; 99US-00436184.
 PA (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
 PI Wands JR, De La Monte SM, Ince N, Carlson RI;
 XX WPI; 2001-329171/34.
 XX N-PSDB; AAF89816.
 XX Diagnosing malignant neoplasm in a mammal, involves contacting mammalian
 PT sample with antibody that binds to human aspartyl beta-hydroxylase
 PT polypeptide to form antigen-antibody complex and detecting the complex.
 PS
 PS Example 7; Page 52; 76pp; English.
 XX The present sequence represents a human insulin receptor substrate (IRS).
 CC Compounds which inhibit IRS also inhibit growth of tumours which
 CC overexpress human aspartyl (asparaginyl) beta-hydroxylase (HAAH) enzyme.
 CC Epidermal growth factor (EGF)-like domains of polypeptides are
 CC hydroxylated by HAAH enzymes. HAAH is used in the method of the
 CC invention. The specification describes a method for diagnosing a
 CC malignant neoplasm in a mammal. The method comprises contacting a body
 CC fluid with an antibody which binds to HAAH polypeptide under complex
 CC forming conditions, and detecting the antigen-antibody complex. The
 CC method is useful for diagnosing and prognosing a malignant neoplasm in a
 CC bodily fluid e.g. central nervous system (CNS)-derived body fluid, blood,
 CC serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal,
 CC where the neoplasm is derived from endodermal tissue and is selected from
 CC colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of
 CC bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic
 CC agent, are useful for killing tumour cells
 XX
 SQ Sequence 1242 AA;
 Query Match 76.5%; Score 39; DB 4; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGSPPC 8
 Db 430 EYGSPPC 436
 RESULT 11
 ABB99797
 ID ABB99797 standard; protein; 1242 AA.
 AC ABB99797;
 DT 07-APR-2003 (first entry)
 XX Amino acid sequence of human insulin receptor substrate-1.
 DE IRS-1; insulin receptor substrate-1; angiogenesis; capillary tube;
 XX endothelial cell; retinopathy; rheumatoid arthritis; Crohn's disease;
 KW atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis;
 KW restenosis; wound healing; peripheral vascular disease; hypertension;
 KW vascular inflammation; Raynaud disease; aneurysm; arterial restenosis;
 KW thrombophlebitis; lymphagitis; lymphodema; ischemia; angina;
 KW myocardial infarction; chronic heart disease; macular degeneration;
 KW osteoporosis; cell multiplication; antitumor.
 XX
 OS Homo sapiens.
 XX
 XX WO2002103014-A2.
 XX 27-DEC-2002.
 PD 14-JUN-2002; 2002WO-FR002067.
 XX 14-JUN-2001; 2001FR-00007805.
 XX (ALMA/) AL-MAHMOOD S.
 PA

XX Al-Mahmood S;
 PI
 XX WPI; 2003-167520/16.
 DR N-PSDB; ABZ23324.
 XX
 XX Angiogenesis-modifying composition, useful for treatment or diagnosis of
 FT e.g. retinopathy, comprises inhibitor of expression of the insulin
 FT receptor substrate-1 gene.
 XX
 XX Disclosure; Page 49-52; 52pp; French.
 PS
 XX The present sequence represents IRS-1 (insulin receptor substrate-1)
 CC polypeptide. IRS-1 is used to produce the compositions of the invention.
 CC The specification describes an angiogenesis-modifying composition,
 CC containing at least one a nucleic acid selected from the gene encoding
 CC IRS-1 or a molecule that inhibits expression of that nucleic acid. The
 CC composition inhibits the formation of capillary tubes by endothelial
 CC cells. The composition is used to treat and diagnose diseases associated
 CC with angiogenesis, particularly retinopathy, rheumatoid arthritis,
 CC Crohn's disease, atherosclerosis, ovarian hyperstimulation, psoriasis,
 CC endometriosis, restenosis after balloon angioplasty, overproduction of
 CC tissue during wound healing, peripheral vascular diseases, hypertension,
 CC vascular inflammation, Raynaud disease, aneurysm, arterial restenosis,
 CC thrombophlebitis, lymphagitis, lymphodema, ischemia, angina, myocardial
 CC infarction, chronic heart disease, (congestive) cardiac insufficiency,
 CC age-related macular degeneration and osteoporosis. It is also used to
 CC prevent cell multiplication, especially as antitumor agents, and as
 CC research reagents for in vitro or in vivo studies on signalling pathways
 XX
 SQ Sequence 1242 AA;
 Query Match 76.5%; Score 39; DB 6; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYGSPPC 8
 Db 430 EYGSPPC 436
 RESULT 12
 ABB72369
 ID ABB72369 standard; protein; 1242 AA.
 XX ABB72369;
 AC ABB72369;
 DT 06-FEB-2003 (first entry)
 XX Human Insulin-receptor substrate-1, IRS-1, Y896F mutant.
 DE
 XX Human; aspartyl (asparaginyl) beta-hydroxylase; HAAH; cytostatic;
 KW immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
 KW brain tumour; glioma; glioblastoma; astrocytoma; haemangioma;
 KW pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer;
 KW liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm;
 KW metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 896 /note= "Wild-type Tyr substituted by Phe"
 FT
 FT
 XX US2002110559-A1.
 XX 15-AUG-2002.
 PD 17-MAY-2001; 2001US-00859604.
 XX 08-NOV-1999; 99US-00436184.
 PR

XX (WAND/) WANDS J R.
PA (DMON/) DE LA MONTE S M.
PA (DEUT/) DEUTCH A H.
PA (GHAN/) GHANBARI H A.
XX
PI Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
XX WPI; 2003-066676/06.
XX
XX Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
PT mammal with detectably-labeled antibody which binds to human aspartyl
XX (asparaginyl) beta-hydroxylase.
XX
XX Example 7; Page; 34pp; English.
XX
XX The invention relates to diagnosing a neoplasm and inhibiting tumor
CC growth in a mammal, using an antibody that binds to human aspartyl
CC (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises
CC contacting a tissue with a detectably-labelled antibody where an increase
CC in level of antibody binding at tissue site compared to the level of
CC binding to normal non-neoplastic tissue indicates the presence of a
CC neoplasm at the tissue site. Inhibiting tumor growth in mammal involves
CC administering the antibody conjugated to a cytotoxic agent to a mammal.
CC Also included are a method of conferring an immune response to a tumour
CC cell in a mammal, by administering the antibody, a method of inducing an
CC HAAH-specific immune response in a mammal, by administering to the mammal
CC an HAAH polypeptide (or a polynucleotide composition encoding the
CC polypeptide, or its degenerate variant), a fragment of HAAH comprising an
CC extracellular domain and lacking a cytoplasmic domain of HAAH, an
CC antibody or its fragment which binds to HAAH (where the antibody is FB50,
CC 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FB50,
CC HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
CC activity or alpha-ketoglutarate binding domain and epidermal growth
CC factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
CC in a mammal, inhibiting tumour growth in a mammal, conferring an immune
CC response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma
CC or haemangioma) in a mammal, for conferring immune response to a
CC pancreatic carcinoma cell and for inducing a HAAH-specific immune
CC response in a mammal. The method is useful for diagnosing malignant
CC neoplasms derived from endodermal tissue, e.g. colon cancer, breast
CC cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
CC method is also useful for diagnosing neoplasms of central nervous system
CC (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial
CC cell origin and metastatic CNS neoplasms, and for diagnosing brain
CC tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
CC present sequence represents a mutant human IRS-1 (insulin receptor
CC substrate-1). IRS-1 mutants were used to elucidate the upregulation of
CC HAAH expression when activated by the IRS-1 signal transduction cascade.
CC Note: The present sequence is not shown in the specification but was
CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
CC the information in Example 7
XX
XX Sequence 1242 AA;
XX
XX Query Match 76.5%; Score 39; DB 6; Length 1242;
XX Best Local Similarity 85.7%; Pred. No. 3.7e+02;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 QYGSPP 8
XX :|||||
XX 430 EYGSPP 436
XX
XX RESULT 13
XX ABG72372
XX ID ABG72372 standard; protein; 1242 AA.
XX
XX AC ABG72372;
XX
XX XX
XX DT 06-FEB-2003 (first entry)
XX
XX DE Human Insulin-receptor substrate-1, IRS-1, Y612P/Y941P mutant.

XX Human, aspartyl (asparaginyl) beta-hydroxylase, HAAH; cytostatic;
XX immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
XX brain tumour; glioma; glioblastoma; astrocytoma; haemangioma;
XX pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer;
XX liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm;
XX metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
XX mutain.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 612 /note= "Wild-type Tyr substituted by Phe"
XX FT Misc-difference 941 /note= "Wild-type Tyr substituted by Phe"
XX FT
XX US2002110559-A1.
XX
XX 15-AUG-2002.
XX
XX 17-MAY-2001; 2001US-00859604.
XX
XX 08-NOV-1999; 99US-00436184.
XX
XX (WAND/) WANDS J R.
XX (DMON/) DE LA MONTE S M.
XX (DEUT/) DEUTCH A H.
XX (GHAN/) GHANBARI H A.
XX
XX Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
XX WPI; 2003-066676/06.
XX
XX Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
PT mammal with detectably-labeled antibody which binds to human aspartyl
XX (asparaginyl) beta-hydroxylase.
XX
XX Example 7; Page; 34pp; English.
XX
XX The invention relates to diagnosing a neoplasm and inhibiting tumour
CC growth in a mammal, using an antibody that binds to human aspartyl
CC (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises
CC contacting a tissue with a detectably-labelled antibody where an increase
CC in level of antibody binding at tissue site compared to the level of
CC binding to normal non-neoplastic tissue indicates the presence of a
CC neoplasm at the tissue site. Inhibiting tumour growth in mammal involves
CC administering the antibody conjugated to a cytotoxic agent to a mammal.
CC Also included are a method of conferring an immune response to a tumour
CC cell in a mammal, by administering the antibody, a method of inducing an
CC HAAH-specific immune response in a mammal, by administering to the mammal
CC an HAAH polypeptide (or a polynucleotide composition encoding the
CC polypeptide, or its degenerate variant), a fragment of HAAH comprising an
CC extracellular domain and lacking a cytoplasmic domain of HAAH, an
CC antibody or its fragment which binds to HAAH (where the antibody is FB50,
CC 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FB50,
CC HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
CC activity or alpha-ketoglutarate binding domain and epidermal growth
CC factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
CC in a mammal, inhibiting tumour growth in a mammal, conferring an immune
CC response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma
CC or haemangioma) in a mammal, for conferring immune response to a
CC pancreatic carcinoma cell and for inducing a HAAH-specific immune
CC response in a mammal. The method is useful for diagnosing malignant
CC neoplasms derived from endodermal tissue, e.g. colon cancer, breast
CC cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
CC method is also useful for diagnosing neoplasms of central nervous system
CC (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial
CC cell origin and metastatic CNS neoplasms, and for diagnosing brain
CC tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
CC present sequence represents a mutant human IRS-1 (insulin receptor
CC substrate-1). IRS-1 mutants were used to elucidate the upregulation of
CC HAAH expression when activated by the IRS-1 signal transduction cascade.
CC Note: The present sequence is not shown in the specification but was
CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
CC the information in Example 7
XX
XX Sequence 1242 AA;
XX
XX Query Match 76.5%; Score 39; DB 6; Length 1242;
XX Best Local Similarity 85.7%; Pred. No. 3.7e+02;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 QYGSPP 8
XX :|||||
XX 430 EYGSPP 436
XX
XX RESULT 13
XX ABG72372
XX ID ABG72372 standard; protein; 1242 AA.
XX
XX AC ABG72372;
XX
XX XX
XX DT 06-FEB-2003 (first entry)
XX
XX DE Human Insulin-receptor substrate-1, IRS-1, Y612P/Y941P mutant.

CC HAAH expression when activated by the IRS-1 signal transduction cascade.
 CC Note: The present sequence is not shown in the specification but was
 CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
 CC the information in Example 7
 XX
 SQ Sequence 1242 AA;

Query Match 76.5%; Score 39; DB 6; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYGSPPC 8
 Db 430 EYGSPPC 436
 :|||||

RESULT 14
 ID ABG72370 standard; protein; 1242 AA.
 XX
 AC ABG72370;
 XX
 DT 06-FEB-2003 (first entry)
 XX Human Insulin-receptor substrate-1, IRS-1, Y1179F mutant.
 DE
 XX Human; aspartyl (asparaginy) beta-hydroxylase; HAAH; cytostatic;
 KW immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
 KW brain tumour; glioma; glioblastoma; astrocytoma; haemangioma;
 KW pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer;
 KW liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm;
 KW metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FH Misc-difference 1179
 FT /note= "Wild-type Tyr substituted by Phe"
 XX
 XX US2002110559-A1.
 XX
 PD 15-AUG-2002.
 XX
 XX 17-MAY-2001; 2001US-00859604.
 XX
 XX 08-NOV-1999; 99US-00436184.
 XX
 XX (WAND/) WANDS J R.
 PA (DMON/) DE LA MONTE S M.
 PA (DEUT/) DEUTCH A H.
 PA (GHAN/) GHANBARI H A.
 XX
 XX Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
 PI
 XX WPI; 2003-066676/06.
 DR
 XX
 FT Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
 FT mammal with detectably-labeled antibody which binds to human aspartyl
 FT (asparaginy) beta-hydroxylase.
 XX
 XX Example 7; Page; 34pp; English.
 PS
 XX The invention relates to diagnosing a neoplasm and inhibiting tumor
 CC growth in a mammal, using an antibody that binds to human aspartyl
 CC (asparaginy) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises
 CC contacting a tissue with a detectably-labeled antibody where an increase
 CC in level of antibody binding at tissue site compared to the level of
 CC binding to normal non-neoplastic tissue indicates the presence of a
 CC neoplasm at the tissue site. Inhibiting tumor growth in mammal involves
 CC administering the antibody conjugated to a cytotoxic agent to a mammal.
 CC Also included are a method of conferring an immune response to a tumour

cell in a mammal, by administering the antibody, a method of inducing an
 HAAH-specific immune response in a mammal, by administering to the mammal
 an HAAH polypeptide (or a polynucleotide composition encoding the
 polypeptide, or its degenerate variant), a fragment of HAAH comprising an
 extracellular domain and lacking a cytoplasmic domain of HAAH, an
 antibody or its fragment which binds to HAAH (where the antibody is FB50,
 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FB50,
 HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
 activity or alpha-ketoglutarate binding domain and epidermal growth
 factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
 in a mammal, inhibiting tumour growth in a mammal, conferring an immune
 response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma
 or haemangioma) in a mammal, for conferring immune response to a
 pancreatic carcinoma cell and for inducing a HAAH-specific immune
 response in a mammal. The method is useful for diagnosing malignant
 neoplasms derived from endodermal tissue, e.g. colon cancer, breast
 cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
 method is also useful for diagnosing neoplasms of central nervous system
 (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial
 cell origin and metastatic CNS neoplasms, and for diagnosing brain
 tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
 present sequence represents a mutant human IRS-1 (insulin receptor
 substrate-1). IRS-1 mutants were used to elucidate the upregulation of
 HAAH expression when activated by the IRS-1 signal transduction cascade.
 Note: The present sequence is not shown in the specification but was
 created by the indexer using the IRS-1 sequence appearing as ABG72368 and
 the information in Example 7

Query Match 76.5%; Score 39; DB 6; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYGSPPC 8
 Db 430 EYGSPPC 436
 :|||||

RESULT 15
 ID ABG72371 standard; protein; 1242 AA.
 XX
 AC ABG72371;
 XX
 DT 06-FEB-2003 (first entry)
 XX Human Insulin-receptor substrate-1, IRS-1, Y896F/Y1179F mutant.
 DE
 XX Human; aspartyl (asparaginy) beta-hydroxylase; HAAH; cytostatic;
 KW immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
 KW brain tumour; glioma; glioblastoma; astrocytoma; haemangioma;
 KW pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer;
 KW liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm;
 KW metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FH Misc-difference 896
 FT /note= "Wild-type Tyr substituted by Phe"
 FT Misc-difference 1179
 FT /note= "Wild-type Tyr substituted by Phe"
 XX
 XX US2002110559-A1.
 XX
 PD 15-AUG-2002.
 XX
 XX 17-MAY-2001; 2001US-00859604.
 XX
 XX 08-NOV-1999; 99US-00436184.

XX (WAND/) WANDS J R.
PA (DMON/) DE LA MONTE S M.
PA (DEUT/) DEUTCH A H.
PA (CHAN/) GHANBARI H A.

XX Wands JR, De La Monte SM, Deutch AH, Ghanbari HA;
PI WPI; 2003-066676/06.

XX DR WPI; 2003-066676/06.

XX Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
PT mammal with detectably-labeled antibody which binds to human aspartyl
PT (asparaginyl) beta-hydroxylase.

XX Example 7; Page; 34pp; English.

XX The invention relates to diagnosing a neoplasm and inhibiting tumour
CC growth in a mammal, using an antibody that binds to human aspartyl
CC (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises
CC contacting a tissue with a detectably-labelled antibody where an increase
CC in level of antibody binding at tissue site compared to the level of
CC binding to normal non-neoplastic tissue indicates the presence of a
CC neoplasm at the tissue site. Inhibiting tumour growth in mammal involves
CC administering the antibody conjugated to a cytotoxic agent to a mammal.
CC Also included are a method of conferring an immune response to a tumour
CC cell in a mammal, by administering the antibody, a method of inducing an
CC HAAH-specific immune response in a mammal, by administering to the mammal
CC an HAAH polypeptide (or a polynucleotide composition encoding the
CC polypeptide, or its degenerate variant), a fragment of HAAH comprising an
CC extracellular domain and lacking a cytoplasmic domain of HAAH, an
CC antibody or its fragment which binds to HAAH (where the antibody is FB50,
CC 86A, 5C7 or 19B), a hybridoma cell line chosen from hybridoma FB50,
CC HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
CC activity or alpha-ketoglutarate binding domain and epidermal growth
CC factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
CC in a mammal, inhibiting tumour growth in a mammal, conferring an immune
CC response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma
CC or haemangioma) in a mammal, for conferring immune response to a
CC pancreatic carcinoma cell and for inducing a HAAH-specific immune
CC response in a mammal. The method is useful for diagnosing malignant
CC neoplasms derived from endodermal tissue, e.g. colon cancer, breast
CC cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
CC method is also useful for diagnosing neoplasms of both neuronal and glial
CC (CNS) e.g. primary malignant CNS neoplasms, and for diagnosing brain
CC cell origin and metastatic CNS neoplasms, and for diagnosing brain
CC tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
CC present sequence represents a mutant human IRS-1 (insulin receptor
CC substrate-1). IRS-1 mutants were used to elucidate the upregulation of
CC HAAH expression when activated by the IRS-1 signal transduction cascade.
CC Note: The present sequence is not shown in the specification but was
CC created by the indexer using the IRS-1 sequence appearing as ABG72368 and
CC the information in Example 7

XX SQ Sequence 1242 AA;

Query Match 76.5%; Score 39; DB 6; Length 1242;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

Search completed: April 21, 2004, 17:33:16
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:33:24 ; Search time 133.826 Seconds

(without alignments)
65.641 Million cell updates/sec

Title: SEQ6

Perfect score: 51

Sequence: 1 qqvgspscs 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

- 1: /cgn2_6/ptodata/2/paa/pctus COMB.pcp:*
- 2: /cgn2_6/ptodata/2/paa/US06 COMB.pcp:*
- 3: /cgn2_6/ptodata/2/paa/US07 COMB.pcp:*
- 4: /cgn2_6/ptodata/2/paa/US08 COMB.pcp:*
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- 28: /cgn2_6/ptodata/2/paa/US102 COMB.pcp:*
- 29: /cgn2_6/ptodata/2/paa/US103 COMB.pcp:*
- 30: /cgn2_6/ptodata/2/paa/US104 COMB.pcp:*
- 31: /cgn2_6/ptodata/2/paa/US106 COMB.pcp:*
- 32: /cgn2_6/ptodata/2/paa/US107 COMB.pcp:*
- 33: /cgn2_6/ptodata/2/paa/US108 COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	100.0	108	1	PCT-US03-00398-49
2	100.0	108	1	PCT-US03-00398-225
3	100.0	108	1	PCT-US03-00398-259
4	100.0	108	1	PCT-US03-00398-375
5	100.0	108	1	PCT-US03-29414-4
6	100.0	108	26	US-10-041-860-49
7	100.0	108	26	US-10-041-860-225
8	100.0	108	26	US-10-041-860-259
9	100.0	108	26	US-10-041-860-375
10	100.0	108	31	US-10-665-383-4
11	94.1	108	22	US-09-791-537-11779
12	88.2	106	22	US-09-791-537-82003
13	88.2	116	22	US-09-791-537-97444
14	79.4	100	22	US-09-791-537-11863
15	78.4	81	22	US-09-791-537-36703
16	78.4	87	1	PCT-US02-32727-5028
17	78.4	87	25	US-09-978-825-5028
18	78.4	87	26	US-10-057-498-5028
19	76.5	74	33	US-60-160-209-3594
20	76.5	74	33	US-60-169-868-4772
21	76.5	81	22	US-09-791-537-36707
22	76.5	86	33	US-60-160-209-4387
23	76.5	86	33	US-60-169-868-6544
24	76.5	89	22	US-09-791-537-127769
25	76.5	90	22	US-09-791-537-36078
26	76.5	92	33	US-60-162-245-3568
27	76.5	100	22	US-09-791-537-133434
28	76.5	102	33	US-60-162-245-2740
29	76.5	102	33	US-60-169-868-5366
30	76.5	142	33	US-60-188-162-5064
31	76.5	212	33	US-60-192-739-2484
32	76.5	212	33	US-60-194-243-1769
33	76.5	212	33	US-60-194-508-1871
34	76.5	234	22	US-09-760-479-604
35	76.5	234	28	US-10-206-008-604
36	76.5	277	22	US-09-760-448A-2273
37	76.5	277	28	US-10-206-664-2273
38	76.5	392	22	US-09-760-446A-1676
39	76.5	392	28	US-10-206-664-1676
40	76.5	412	27	US-10-104-047-3475
41	76.5	530	33	US-60-452-680-19149
42	76.5	669	1	PCT-US03-28227-3972
43	76.5	691	22	US-09-791-537-885
44	76.5	695	1	PCT-US03-28227-3973
45	76.5	695	22	US-09-791-537-71531

ALIGNMENTS

RESULT 1
PCT-US03-00398-49
; Sequence 49, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: AGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.

; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gad
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: AGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens

Sequence 49, Appl
Sequence 225, App
Sequence 259, App
Sequence 375, App
Sequence 4, Appl
Sequence 49, Appl
Sequence 225, App
Sequence 259, App
Sequence 375, App
Sequence 4, Appl
Sequence 11779, A
Sequence 82003, A
Sequence 97444, A
Sequence 11863, A
Sequence 36703, A
Sequence 5028, Ap
Sequence 5028, Ap
Sequence 5028, Ap
Sequence 3594, Ap
Sequence 4772, Ap
Sequence 36707, A
Sequence 4387, Ap
Sequence 6544, Ap
Sequence 127769, A
Sequence 36078, A
Sequence 3568, Ap
Sequence 133434, A
Sequence 2740, Ap
Sequence 5366, Ap
Sequence 5064, Ap
Sequence 2484, Ap
Sequence 1769, Ap
Sequence 1871, Ap
Sequence 604, App
Sequence 604, App
Sequence 2273, Ap
Sequence 2273, Ap
Sequence 1676, Ap
Sequence 1676, Ap
Sequence 3475, Ap
Sequence 19149, A
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Sequence 3973, Ap
Sequence 71531, A

PCT-US03-00398-49

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
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Db 90 QOYGSPPCS 98

RESULT 2

PCT-US03-00398-225
; Sequence 225, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-225

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
| | | | | | | | | |
Db 90 QOYGSPPCS 98

RESULT 3

PCT-US03-00398-259
; Sequence 259, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-259

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
| | | | | | | | | |
Db 90 QOYGSPPCS 98

RESULT 4

PCT-US03-00398-375
; Sequence 375, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-00398-375

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
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Db 90 QOYGSPPCS 98

RESULT 5

PCT-US03-29414-4
; Sequence 4, Application PC/TUS0329414
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: FLOERGE, Juergen
; APPLICANT: GAZIT, Gadi
; APPLICANT: KEYI, Bruce
; APPLICANT: LAROCHE, William, J.
; APPLICANT: LICHENSTEIN, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052VPC
; CURRENT APPLICATION NUMBER: PCT/US03/29414
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US03-29414-4

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSPPCS 9
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Db 90 QOYGSPPCS 98

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RESULT 6
US-10-041-860-49
; Sequence 49, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSPPCS 9
Db 90 QQYGSPPCS 98

RESULT 7
US-10-041-860-225
; Sequence 225, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-225

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSPPCS 9
Db 90 QQYGSPPCS 98

RESULT 8
US-10-041-860-259
; Sequence 259, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSPPCS 9
Db 90 QQYGSPPCS 98

RESULT 9
US-10-041-860-375
; Sequence 375, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-375

Query Match      100.0%; Score 51; DB 26; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSPPCS 9
Db 90 QQYGSPPCS 98

RESULT 10
US-10-665-383-4
; Sequence 4, Application US/10665383
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Laroche, William
; APPLICANT: Lichenstein, Henri

```


; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
 ; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
 ; FILE REFERENCE: ABGNIX.052A
 ; CURRENT APPLICATION NUMBER: US/10/665,383
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/411,137
 ; PRIOR FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-665-383-4

Query Match 100.0%; Score 51; DB 31; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSPPCS 9
 Db 90 QQYGSPPCS 98

RESULT 11
 US-09-791-537-11779
 ; Sequence 11779, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11779
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-11779

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 Best Local Similarity 88.9%; Pred. No. 3.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSPPCS 9
 Db 82 QQYGSPPCS 90

RESULT 12
 US-09-791-537-82003
 ; Sequence 82003, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 82003
 ; LENGTH: 109
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-82003

Query Match 88.2%; Score 45; DB 22; Length 109;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSPPCS 9
 Db 90 QQYGSPPCS 98

RESULT 13
 US-09-791-537-97444
 ; Sequence 97444, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 97444
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-97444

Query Match 88.2%; Score 45; DB 22; Length 116;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSPPCS 9
 Db 90 QQYGSPPCS 98

RESULT 14
 US-09-791-537-11863
 ; Sequence 11863, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 11863
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-11863

Query Match 79.4%; Score 40.5; DB 22; Length 100;
 Best Local Similarity 90.0%; Pred. No. 75;
 Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QQYGSPPCS 9
 Db 81 QQYGSPPCS 90

RESULT 15
 US-09-791-537-36703
 ; Sequence 36703, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek

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; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36703
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-36703

Query Match      78.4%; Score 40; DB 22; Length 81;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QYGSPPCS 9
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DB      71 QYGSPPYS 79

Search completed: April 21, 2004, 17:57:25
Job time : 134.826 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: April 21, 2004, 17:34:09 ; Search time 6.3913 Seconds
(without alignments)
39.310 Million cell updates/sec
Title: SEQ6
Perfect score: 51
Sequence: 1 qygsppc 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 198209 seqs, 27915599 residues
Total number of hits satisfying chosen parameters: 198209
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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Query Match Length DB ID Description
1 39 76.5 1231 1 PCT-US03-34861-3 Sequence 3, Appli
2 39 76.5 1242 1 PCT-US03-34861-1 Sequence 1, Appli
3 38 74.5 9 6 US-10-663-244-32 Sequence 32, Appli
4 38 74.5 9 6 US-10-630-009-52 Sequence 52, Appli
5 38 74.5 9 6 US-10-630-009-56 Sequence 56, Appli
6 38 74.5 96 6 US-10-612-497A-87 Sequence 87, Appli
7 38 74.5 105 6 US-10-630-009-3 Sequence 3, Appli
8 38 74.5 105 6 US-10-630-009-7 Sequence 7, Appli
9 38 74.5 108 1 PCT-US03-36894-123 Sequence 123, Appli
10 38 74.5 108 6 US-10-663-244-9 Sequence 9, Appli
11 38 74.5 109 1 PCT-US03-38384A-27 Sequence 27, Appli
12 38 74.5 109 1 PCT-US03-38384A-28 Sequence 28, Appli
13 38 74.5 109 1 PCT-US03-38234A-4 Sequence 4, Appli
14 38 74.5 109 1 PCT-US03-38234A-6 Sequence 6, Appli
15 38 74.5 109 1 PCT-US03-38234A-14 Sequence 14, Appli
16 38 74.5 109 1 PCT-US03-38234A-210 Sequence 210, Appli
17 38 74.5 109 6 US-10-487-525-64 Sequence 64, Appli
18 38 74.5 110 1 PCT-US03-38234A-16 Sequence 16, Appli
19 38 74.5 110 1 PCT-US03-38234A-213 Sequence 213, Appli
20 38 74.5 130 6 US-10-693-629-46 Sequence 46, Appli
21 38 74.5 215 1 PCT-US03-36894-122 Sequence 122, Appli
22 38 74.5 384 6 US-10-275-027A-804 Sequence 804, Appli
23 38 74.5 384 6 US-10-275-027A-805 Sequence 805, Appli
24 38 74.5 384 6 US-10-275-027A-806 Sequence 806, Appli
25 38 74.5 384 6 US-10-275-027A-807 Sequence 807, Appli
26 36.5 71.6 236 6 US-10-800-250-34 Sequence 34, Appli

Sequence 38, Appli
Sequence 7250, Ap
Sequence 4272, Ap
Sequence 55, Appl
Sequence 132, App
Sequence 150, App
Sequence 6, Appli
Sequence 88, Appli
Sequence 19, Appl
Sequence 92, Appl
Sequence 485, App
Sequence 14, Appl
Sequence 65, Appl
Sequence 11, Appl
Sequence 24, Appl
Sequence 34251, A
Sequence 32361, A
Sequence 118, App

ALIGNMENTS

RESULT 1
PCT-US03-34861-3
; Sequence 3, Application PC/TUS0334861
; GENERAL INFORMATION:
; APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
; APPLICANT: POLAKIEWICZ, Roberto
; APPLICANT: LI, Yu
; APPLICANT: WU, Jiong
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR PHOSPHORYLATED IRS-1/2 (Ser1101/Ser1149)
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CST-209 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/34861
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/422,409
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1231
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-34861-3

Query Match 76.5%; Score 39; DB 1; Length 1231;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QYGSPPC 8
Db 425 EYGSPPC 431

RESULT 2
PCT-US03-34861-1
; Sequence 1, Application PC/TUS0334861
; GENERAL INFORMATION:
; APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
; APPLICANT: POLAKIEWICZ, Roberto
; APPLICANT: LI, Yu
; APPLICANT: WU, Jiong
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR PHOSPHORYLATED IRS-1/2 (Ser1101/Ser1149)
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CST-209 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/34861
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/422,409
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1

Query Match 76.5%; Score 39; DB 1; Length 1231;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QYGSPPC 8
Db 425 EYGSPPC 431

; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-34861-1

Query Match 76.5%; Score 39; DB 1; Length 1242;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPC 8
Db 430 EYGSPPC 436

RESULT 3

US-10-663-244-32

; Sequence 32, Application US/10663244
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-32

Query Match 74.5%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGSPP 7
Db 1 QYGSPP 7

RESULT 4

US-10-630-009-52

; Sequence 52, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-52

Query Match 74.5%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QYGSPP 7
Db 1 QYGSPP 7

RESULT 5

US-10-630-009-56

; Sequence 56, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-56

Query Match 74.5%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGSPP 7
Db 1 QYGSPP 7

RESULT 6

US-10-612-497A-87

; Sequence 87, Application US/10612497A
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/10/612,497A
; CURRENT FILING DATE: 2003-07-01
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-497A-87

Query Match 74.5%; Score 38; DB 6; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYGSPP 7
Db 90 QYGSPP 96

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RESULT 7
US-10-630-009-3
; Sequence 3, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-3

Query Match          74.5%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 83 QOYGSSP 89

RESULT 8
US-10-630-009-7
; Sequence 7, Application US/10630009
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Ditzel, H.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-7

Query Match          74.5%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 83 QOYGSSP 89

RESULT 9
PCT-US03-36894-123
; Sequence 123, Application PC/TUS0336894
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 54 CIP PCT (1087-2 CIP PCT)
; CURRENT APPLICATION NUMBER: PCT/US03/36894

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; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain variable region
PCT-US03-36894-123

Query Match          74.5%; Score 38; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 90 QOYGSSP 96

RESULT 10
US-10-663-244-9
; Sequence 9, Application US/10663244
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Rachel Baribault
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-9

Query Match          74.5%; Score 38; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 90 QOYGSSP 96

RESULT 11
PCT-US03-38384A-27
; Sequence 27, Application PC/TUS0338384A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: OWENS, Samuel, M.
; APPLICANT: CAREOL, Frank, I.
; APPLICANT: ABRAHAM, Philip
; APPLICANT: GUNNELLE, Melinda, G.
; APPLICANT: HAAK-FRENDTSCHO, Mary
; APPLICANT: FENG, Xiao
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071VFC

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; CURRENT APPLICATION NUMBER: PCT/US03/38384A
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-38384A-27

Query Match          74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 90 QOYGSSP 96

RESULT 12
PCT-US03-38384A-28
; Sequence 28, Application PC/TUS0338384A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: OWENS, Samuel, M.
; APPLICANT: CARROL, Frank, I.
; APPLICANT: ABRAHAM, Philip
; APPLICANT: GUNNELL, Melinda, G.
; APPLICANT: HAAK-FRENDSCHO, Mary
; APPLICANT: FENG, Xiao
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38384A
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-38384A-28

Query Match          74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 90 QOYGSSP 96

PCT-US03-38234A-6
; Sequence 6, Application PC/TUS0338234A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: LEXICON GENETICS INCORPORATED
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38234A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/38234
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234A-6

Query Match          74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 90 QOYGSSP 96

PCT-US03-38234A-14
; Sequence 14, Application PC/TUS0338234A
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: LEXICON GENETICS INCORPORATED
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF
; FILE REFERENCE: ABGENIX.072VPC
; CURRENT APPLICATION NUMBER: PCT/US03/38234A
; CURRENT FILING DATE: 2003-02-19

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; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US03/38234
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234A-14

Query Match 74.5%; Score 38; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3-2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGGSP 7
|||
Db 90 QQYGGSP 96

Search completed: April 21, 2004, 17:58:26
Job time : 6.3913 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:28:28 ; Search time 10.8261 Seconds
(without alignments)
42.918 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 qyggspecs 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCITUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	39	76.5	1242	4	US-09-508-691-1
6	39	76.5	1243	2	US-08-557-139-2
7	38	74.5	9	2	US-08-350-260A-503
8	38	74.5	9	3	US-09-042-353-362
9	38	74.5	9	4	US-08-758-417A-210
10	38	74.5	9	4	US-09-104-337A-503
11	38	74.5	96	4	US-09-472-087-87
12	38	74.5	107	1	US-08-107-669D-14
13	38	74.5	107	1	US-08-472-788A-14
14	38	74.5	107	2	US-08-477-531B-14
15	38	74.5	107	2	US-08-652-558-49
16	38	74.5	107	2	US-08-082-842A-14
17	38	74.5	107	4	US-08-635-109-7
18	38	74.5	108	1	US-08-488-113B-150
19	38	74.5	108	1	US-08-477-484B-150
20	38	74.5	108	2	US-08-646-360-150
21	38	74.5	108	2	US-08-232-081B-42
22	38	74.5	108	3	US-08-839-765-150
23	38	74.5	108	3	US-09-136-389-150
24	38	74.5	108	3	US-09-240-274-178
25	38	74.5	108	4	US-09-610-838-150
26	38	74.5	108	4	US-09-711-485-150
27	38	74.5	112	1	US-08-276-852-151

28	38	74.5	112	1	US-08-899-575-151	Sequence 151, App
29	38	74.5	112	1	US-08-899-575-151	Sequence 151, App
30	38	74.5	112	5	PCT-US95-08743-151	Sequence 151, App
31	38	74.5	116	1	US-08-053-131-183	Sequence 183, App
32	38	74.5	116	2	US-08-096-762-183	Sequence 183, App
33	38	74.5	116	3	US-09-042-353-46	Sequence 46, Appl
34	38	74.5	116	4	US-08-758-417A-311	Sequence 311, Appl
35	38	74.5	150	3	US-08-862-124-5	Sequence 5, Appl1
36	38	74.5	226	4	US-09-456-090A-38	Sequence 38, Appl
37	38	74.5	226	4	US-09-456-090A-42	Sequence 42, Appl
38	38	74.5	226	4	US-09-456-090A-50	Sequence 50, Appl
39	38	74.5	226	4	US-09-456-090A-72	Sequence 72, Appl
40	38	74.5	226	4	US-09-456-090A-74	Sequence 74, Appl
41	38	74.5	226	4	US-09-456-090A-80	Sequence 80, Appl
42	38	74.5	226	4	US-09-456-090A-86	Sequence 86, Appl
43	38	74.5	235	3	US-08-812-586-16	Sequence 16, Appl
44	38	74.5	235	4	US-09-535-832A-17	Sequence 17, Appl
45	38	74.5	239	3	US-08-812-586-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-094-948A-29
; Sequence 29; Application US/08094948A
; Patent No. 5621075
; GENERAL INFORMATION:
; APPLICANT: Kahn, C. Ronald
; APPLICANT: White, Morris F.
; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/094,948A
; FILING DATE: 21-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,982
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-013DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-094-948A-29

Query Match 76.5%; Score 39; DB 1; Length 1155;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGS8PC 8
Db 385 EYGS8PC 391

RESULT 2
 PCT-US96-09319-29
 ; Sequence 29, Application PC/TUS9609319
 ; GENERAL INFORMATION:
 ; APPLICANT: Kahn, C. Ronald
 ; APPLICANT: White, Morris F.
 ; APPLICANT: Rothenberg, Paul Louis
 ; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lahive & Cockfield
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02109
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/09319
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/094,948
 ; FILING DATE: 21-JULY-1993
 ; APPLICATION NUMBER: US 07/643,982
 ; FILING DATE: 18-JAN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Myers, Louis (PLM)
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: JDP-013DV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1155 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US96-09319-29

Query Match 76.5%; Score 39; DB 5; Length 1155;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYGSPPC 8
 Db 385 EYGSPPC 391

RESULT 3
 US-08-317-310A-15
 ; Sequence 15, Application US/08317310A
 ; Patent No. 5858701
 ; GENERAL INFORMATION:
 ; APPLICANT: WHITE, Morris F.
 ; APPLICANT: SUN, Xiao Jian
 ; APPLICANT: PIERCE, Jacalyn H.
 ; TITLE OF INVENTION: THE IRS FAMILY OF GENES
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/317,310A
 ; FILING DATE: 03-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Louis Myers
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: JDP-022
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-08-317-310A-15

Query Match 76.5%; Score 39; DB 2; Length 1234;
 Best Local Similarity 85.7%; Pred. No. 86;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYGSPPC 8
 Db 425 EYGSPPC 431

RESULT 4
 PCT-US95-13041-15
 ; Sequence 15, Application PC/TUS9513041
 ; GENERAL INFORMATION:
 ; APPLICANT: WHITE, Morris F.
 ; APPLICANT: SUN, Xiao Jian
 ; APPLICANT: PIERCE, Jacalyn H.
 ; TITLE OF INVENTION: THE IRS FAMILY OF GENES
 ; NUMBER OF SEQUENCES: 83
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13041
 ; FILING DATE: Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/317,310
 ; FILING DATE: 03-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Louis Myers
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: JDP-022PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide


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; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 503:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-503

Query Match 74.5%; Score 38; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 1 QQYGSSP 7

RESULT 8
US-09-042-353-362
; Sequence 362, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301

```

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; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-042-353-362

Query Match 74.5%; Score 38; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
Db 1 QQYGSSP 7

RESULT 9
US-08-758-417A-210
; Sequence 210, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-08-758-417A-210

Query Match 74.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
| | | | |
Db 1 QQYGSSP 7

RESULT 10
US-09-104-337A-503
Sequence 503, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 503:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 503:
US-09-104-337A-503

Query Match 74.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYGSSP 7
| | | | |
Db 1 QQYGSSP 7

RESULT 11
US-09-472-087-87
Sequence 87, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 96
TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-472-087-87

Query Match      74.5%; Score 38; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      90 QQYGSSP 96

RESULT 12
US-08-107-669D-14
; Sequence 14, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; NAME: Michele A. Cimbala
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-14

Query Match      74.5%; Score 38; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      89 QQYGSSP 95

RESULT 13
US-08-472-788A-14
; Sequence 14, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; NAME: Cimbala, Michele A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-14

Query Match      74.5%; Score 38; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QQYGSSP 7
Db      89 QQYGSSP 95

RESULT 14
US-08-477-531B-14
; Sequence 14, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA: PCT/US92/10906
; APPLICATION NUMBER: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 13-DEC-1991
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-14

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Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOYGSSP 7
Db 89 QOYGSSP 95

```

RESULT 15

```

US-08-652-558-49
; Sequence 49, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-49

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Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QOYGSSP 7
Db 88 QOYGSSP 94

```

```

Search completed: April 21, 2004, 17:40:06
Job time : 11.8261 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:27:33 ; Search time 8.21739 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: SEQ6
Perfect score: 51
Sequence: 1 qoygsspcs 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	88.2	109	2 F30601	Ig kappa chain V-I
2	39	76.5	109	1 K3HUGO	Ig kappa chain V-I
3	39	76.5	1231	2 S30185	insulin receptor s
4	39	76.5	1235	1 S16948	insulin receptor s
5	39	76.5	1240	2 JCS209	insulin receptor s
6	39	76.5	1242	2 JS0670	alpha-2-macroglob
7	39	76.5	4543	1 A53102	Ig kappa chain V r
8	38	74.5	54	2 A25521	Ig kappa chain V r
9	38	74.5	91	2 S37520	Ig kappa chain V r
10	38	74.5	91	2 S67940	Ig kappa chain V r
11	38	74.5	92	2 S37524	Ig kappa chain V r
12	38	74.5	92	2 S37513	Ig kappa chain V r
13	38	74.5	92	2 S37519	Ig kappa chain V r
14	38	74.5	92	2 S37517	Ig kappa chain V r
15	38	74.5	92	2 S37510	Ig kappa chain V r
16	38	74.5	92	2 S37518	Ig kappa chain V r
17	38	74.5	93	2 S37526	Ig kappa chain V r
18	38	74.5	93	2 S37528	Ig kappa chain V r
19	38	74.5	93	2 S37501	Ig kappa chain V r
20	38	74.5	96	2 A30601	Ig kappa chain V-I
21	38	74.5	108	1 K3HUB6	Ig kappa chain V-I
22	38	74.5	108	2 C30608	Ig kappa chain V-I
23	38	74.5	108	2 B30608	Ig kappa chain V r
24	38	74.5	108	2 H44151	Ig kappa chain V r
25	38	74.5	109	1 K3HUSI	Ig kappa chain V-I
26	38	74.5	109	1 K3HUTI	Ig kappa chain V-I
27	38	74.5	109	2 PH0963	Ig kappa chain V r
28	38	74.5	109	2 G30601	Ig kappa chain V-I
29	38	74.5	109	2 B30601	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

F30601
Ig kappa chain V-III region (Neu) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: F30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solor
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: F30601
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <CON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-91/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 45; DB 2; Length 109;
Best Local Similarity 77.8%; Pred.No. 0.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSPCS 9
DB 90 QOYGASPCPT 98
|||||:|||||

RESULT 2

K3HUGO
Ig kappa chain V-III region (Gol) - human
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01893
R:Newkirk, M.; Chen, P.P.; Carson, D.; Posnett, D.; Capra, J.D.
Mol. Immunol. 23, 239-244, 1986
A:Title: Amino acid sequence of a light chain variable region of a human rheumatoid fact
A:Reference number: A01893; MUID:86230578; PMID:3086710
A:Accession: A01893
A:Molecule type: protein
A:Residues: 1-109 <NEW>
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-91/Domain: immunoglobulin homology <IMM>
P:23-89/Disulfide bonds: #status predicted

```

Query Match      76.5%; Score 39; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYGSPPCS 9
Db 90 QYGSPPCS 98

RESULT 3
S30185
insulin receptor substrate 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C/Accession: S30185; S43514
R/Keller, S.R.; Aebersold, R.; Garner, C.W.; Lienhard, G.E.
Biochim. Biophys. Acta 1172, 323-326, 1993
A/Title: The insulin-elicited 160 kDa phosphotyrosine protein in mouse adipocytes is an
A/Reference number: S30185; MUID:93192326; PMID:8448209
A/Accession: S30185
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1231 <KEL>
A/Cross-references: EMBL:X59732; NID:G297913; PIDN:CAA49378.1; PID:G297914
R/Araki, E.; Haag III, B.L.; Kahn, C.R.
Biochim. Biophys. Acta 1221, 353-356, 1994
A/Title: Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete seq
A/Reference number: S43514; MUID:94220494; PMID:8167159
A/Accession: S43514
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1037, 'AS', 1038-1179, 'H', 1181-1231 <ARA>
A/Cross-references: EMBL:L24563; NID:G407993; PIDN:AAA39335.1; PID:G407994
C/Superfamily: Insulin receptor substrate IRS-1; pleckstrin repeat homology
F/11-113/Domain: pleckstrin repeat homology <PLK>

Query Match      76.5%; Score 39; DB 2; Length 1231;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 8
Db 425 EYGSPPCS 431

RESULT 4
S16948
insulin receptor substrate IRS-1 - rat
N/Alternate names: insulin receptor substrate pp185
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C/Accession: S16948; A39811
R/Sun, X.J.; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wilden, P.A.; Cahill,
Nature 352, 73-77, 1991
A/Title: Structure of the insulin receptor substrate IRS-1 defines a unique signal trans
A/Reference number: S16948; MUID:91287824; PMID:1648180
A/Accession: S16948
A/Molecule type: mRNA
A/Residues: 1-1235 <SUN>
A/Cross-references: EMBL:X59375; NID:G56503; PIDN:CAA41264.1; PID:G56504
R/Rothenberg, P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
J. Biol. Chem. 266, 8302-8311, 1991
A/Title: Purification and partial sequence analysis of pp185, the major cellular substra
A/Reference number: A39811; MUID:91217066; PMID:2022647
A/Accession: A39811
A/Molecule type: protein
A/Residues: 44-51; 173-178; 223-243; 489-506; 635-646; 871-882, 'I', 884, 'X', 886-888; 932-936, 'X'
A/Note: The phosphotyrosine residue was not identified
C/Comment: This protein and the beta chain of the insulin receptor itself are the major
C/Comment: Phosphorylation of this protein in response to insulin is maximal at 30 second
insulin.
C/Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C/Keywords: Phosphoprotein; signal transduction

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F/11-113/Domain: pleckstrin repeat homology <PLK>
F/872-891/Region: glutamine-rich

Query Match      76.5%; Score 39; DB 1; Length 1235;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 8
Db 425 EYGSPPCS 431

RESULT 5
JC5209
insulin receptor substrate 1 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 16-Jul-1999
C/Accession: JC5209; PC4305
R/Raouls, M.; Taylor, S.I.; Reitman, M.
Gene 178, 51-55, 1996
A/Title: Cloning of the chicken insulin receptor substrate 1 gene.
A/Reference number: JC5209; MUID:97080546; PMID:8921891
A/Accession: JC5209
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-1240 <RAO>
A/Cross-references: GB:U43502; NID:G1685084; PIDN:AAC60050.1; PID:G1685085
A/Accession: PC4305
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <TA2>
C/Comment: This protein acts as a docking protein and mediates multiple interactions amo
C/Genetics:
A/Gene: Isr-1
C/Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C/Keywords: phosphoprotein
F/11-112/Domain: pleckstrin repeat homology <PLK>
F/463,549,610,630,660,730,940,987,1010/Binding site: phosphate (Tyr) (covalent) #status

Query Match      76.5%; Score 39; DB 2; Length 1240;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYGSPPCS 8
Db 428 EYGSPPCS 434

RESULT 6
JS0670
insulin receptor substrate-1 - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 23-Aug-1996 #text_change 16-Jul-1999
C/Accession: JS0670; JS0670; FN0678
R/Araki, E.; Sun, X.J.; Haag, B.L.; Chuang, L.; Zhang, Y.; Yang-Feng, T.L.; White, M.; K
Diabetes 42, 1041-1054, 1993
A/Title: Human skeletal muscle insulin receptor substrate-1. Characterization of the CDN
A/Reference number: JS0670; MUID:93292738; PMID:8513971
A/Accession: JS0670
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1242 <RS>
A/Cross-references: GB:S62539; NID:G386256; PIDN:AAB27175.1; PID:G386257
R/Nishiyama, M.; Wands, J.R.
Biochem. Biophys. Res. Commun. 183, 280-285, 1992
A/Title: Cloning and increased expression of an insulin receptor substrate-1-like gene i
A/Reference number: JS0670; MUID:92181456; PMID:1311924
A/Accession: JS0670
A/Molecule type: mRNA
A/Residues: 1-134, 'G', 135-361, 'R', 363-383, 'R', 385-1242 <NIS>
A/Cross-references: GB:S85963; NID:G246465; PIDN:AA21608.1; PID:G246466
A/Experimental source: hepatocellular carcinoma cell line FOCUS
R/Smith, L.K.; Bradshaw, M.; Croall, D.E.; Garner, C.W.

```


Biochem. Biophys. Res. Commun. 196, 767-772, 1993
 A>Title: The insulin receptor substrate (IRS-1) is a PEST protein that is susceptible to
 A:Reference number: P06678; PMID:94059102; PMID:8240352
 A:Accession: P06678
 A:Molecule type: protein
 A:Residues: 1-14,338-353;411-439;538-545,'V',547-567;656-697;724-758;932-943;1028-1056;1
 C:Comment: This protein appears to be the major substrate for insulin-stimulated tyrosin
 o dock various proteins containing the phosphotyrosine-binding Src-homology domain 2 (SH
 C:Comment: This protein contains at least 11 PEST regions, which suggests rapid turnover
 C:Genetics:
 A:Gene: GDB:IRSI
 A:Cross-references: GDB:133974; OMIM:147545
 A:Map position: 2q36-2q36
 A:Introns: #status absent
 C:Superfamily: Insulin receptor substrate IRS-1; pleckstrin repeat homology
 C:Keywords: ATP; pleckstrin repeat homology <PLK>
 F:11-113/Domain: pleckstrin repeat homology <PLK>
 F:46-525,551,612,662,732,941,989,1012/Binding site: phosphate (Tyr) (covalent) #statu
 F:78,527,1100,1223/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
 F:161/Binding site: ATP (Lys) #status predicted
 F:189,323,441,624,636,795,920,984,1084,1218/Binding site: phosphate (Ser) (covalent) (by
 F:300,351,774/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre

Query Match 76.5%; Score 39; DB 2; Length 1242;
 Best Local Similarity 85.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QVGSPPC 8
 Db 430 EYGSPPC 436
 :|||||

RESULT 7
 A53102
 Alpha-2-macroglobulin receptor precursor - chicken
 N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein recepto
 C:Species: Gallus gallus (chicken)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 22-Jun-1999
 R:Nimf, J.; Stefani, S.; Bilous, P.T.; Schneider, W.J.
 J. Biol. Chem. 269, 212-219, 1994
 A>Title: The somatic cell-specific low density lipoprotein receptor-related protein of b
 A:Reference number: A53102; PMID:94103212; PMID:7506255
 A:Accession: A53102
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-4543 <NIM>
 A:Cross-references: GB:X74904; NID:9438006; PIDN:CAAS2870.1; PID:9438007
 C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
 d protein.
 C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-3942,3943-4543/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
 F:29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:43-470/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:117-150/Domain: EGF homology <EG1>
 F:156-190/Domain: EGF homology <EG2>
 F:200-241/Domain: LDL receptor YWTD-containing repeat homology <YW01>
 F:242-283/Domain: LDL receptor YWTD-containing repeat homology <YW02>
 F:294-336/Domain: LDL receptor YWTD-containing repeat homology <YW03>
 F:337-380/Domain: LDL receptor YWTD-containing repeat homology <YW04>
 F:381-422/Domain: LDL receptor YWTD-containing repeat homology <YW05>
 F:423-470/Domain: LDL receptor YWTD-containing repeat homology <YW06>
 F:480-521/Domain: EGF homology <EG3>
 F:573-615/Domain: LDL receptor YWTD-containing repeat homology <YW07>
 F:616-661/Domain: LDL receptor YWTD-containing repeat homology <YW08>
 F:662-712/Domain: LDL receptor YWTD-containing repeat homology <YW09>
 F:713-754/Domain: LDL receptor YWTD-containing repeat homology <YW10>
 F:755-797/Domain: LDL receptor YWTD-containing repeat homology <YW11>
 F:805-840/Domain: EGF homology <EG4>
 F:852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:934-969/Domain: LDL receptor ligand-binding repeat homology <LDL5>
 F:974-1009/Domain: LDL receptor ligand-binding repeat homology <LDL6>
 F:1013-1049/Domain: LDL receptor ligand-binding repeat homology <LDL7>
 F:1060-1095/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:1102-1138/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDL10>
 F:1183-1219/Domain: EGF homology <EG5>
 F:1225-1259/Domain: EGF homology <EG6>
 F:1267-1306/Domain: LDL receptor YWTD-containing repeat homology <YW12>
 F:1307-1353/Domain: LDL receptor YWTD-containing repeat homology <YW13>
 F:1354-1396/Domain: LDL receptor YWTD-containing repeat homology <YW14>
 F:1397-1443/Domain: LDL receptor YWTD-containing repeat homology <YW15>
 F:1444-1486/Domain: LDL receptor YWTD-containing repeat homology <YW16>
 F:1487-1529/Domain: LDL receptor YWTD-containing repeat homology <YW17>
 F:1538-1576/Domain: EGF homology <EG7>
 F:1581-1624/Domain: LDL receptor YWTD-containing repeat homology <YW18>
 F:1625-1667/Domain: LDL receptor YWTD-containing repeat homology <YW19>
 F:1668-1711/Domain: LDL receptor YWTD-containing repeat homology <YW20>
 F:1712-1751/Domain: LDL receptor YWTD-containing repeat homology <YW21>
 F:1752-1794/Domain: LDL receptor YWTD-containing repeat homology <YW22>
 F:1795-1842/Domain: LDL receptor YWTD-containing repeat homology <YW23>
 F:1846-1882/Domain: EGF homology <EG8>
 F:1930-1972/Domain: LDL receptor YWTD-containing repeat homology <YW24>
 F:1973-2015/Domain: LDL receptor YWTD-containing repeat homology <YW25>
 F:2016-2059/Domain: LDL receptor YWTD-containing repeat homology <YW26>
 F:2060-2101/Domain: LDL receptor YWTD-containing repeat homology <YW27>
 F:2102-2147/Domain: EGF homology <EG9>
 F:2155-2190/Domain: LDL receptor YWTD-containing repeat homology <YW28>
 F:2195-2237/Domain: LDL receptor YWTD-containing repeat homology <YW29>
 F:2247-2288/Domain: LDL receptor YWTD-containing repeat homology <YW30>
 F:2338-2382/Domain: LDL receptor YWTD-containing repeat homology <YW31>
 F:2383-2423/Domain: LDL receptor YWTD-containing repeat homology <YW32>
 F:2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW33>
 F:2476-2511/Domain: EGF homology <EG10>
 F:2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:2560-2594/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2599-2633/Domain: LDL receptor ligand-binding repeat homology <LDL10>
 F:2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDL11>
 F:2690-2724/Domain: LDL receptor ligand-binding repeat homology <LDL12>
 F:2732-2767/Domain: LDL receptor ligand-binding repeat homology <LDL13>
 F:2772-2810/Domain: LDL receptor ligand-binding repeat homology <LDL14>
 F:2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDL15>
 F:2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDL16>
 F:2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDL17>
 F:2941-2977/Domain: EGF homology <EG11>
 F:2983-3018/Domain: LDL receptor YWTD-containing repeat homology <YW34>
 F:3026-3065/Domain: LDL receptor YWTD-containing repeat homology <YW35>
 F:3086-3110/Domain: LDL receptor YWTD-containing repeat homology <YW36>
 F:3111-3153/Domain: LDL receptor YWTD-containing repeat homology <YW37>
 F:3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW38>
 F:3239-3281/Domain: LDL receptor YWTD-containing repeat homology <YW39>
 F:3291-3327/Domain: EGF homology <EG12>
 F:3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL18>
 F:3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDL19>
 F:3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDL20>
 F:3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDL21>
 F:3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDL22>
 F:3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDL23>
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 F:3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDL25>
 F:3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDL26>
 F:3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDL27>
 F:3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDL28>
 F:3783-3820/Domain: EGF homology <EG14>
 F:3826-3859/Domain: EGF homology <EG15>
 F:3866-3909/Domain: LDL receptor YWTD-containing repeat homology <YW40>
 F:3910-3968/Domain: LDL receptor YWTD-containing repeat homology <YW41>
 F:3943-4543/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
 F:755-797/Domain: 85K chain extracellular #status predicted <85K>
 F:3969-4011/Domain: LDL receptor YWTD-containing repeat homology <YW42>
 F:4012-4055/Domain: LDL receptor YWTD-containing repeat homology <YW43>

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F:4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YH44>
F:4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YH45>
F:4150-4181/Domain: EGF homology <EG16>
F:4199-4230/Domain: EGF homology <EG17>
F:4235-4266/Domain: EGF homology <EG18>
F:4271-4302/Domain: EGF homology <EG19>
F:4307-4338/Domain: EGF homology <EG20>
F:4343-4373/Domain: EGF homology <EG21>
F:4376-4408/Domain: EGF homology <EG22>
F:4421-4443/Domain: transmembrane #status predicted <TM>
F:4444-4543/Domain: intracellular #status predicted <INT>
F:116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643
3485,3659,3786,3837,3952,4074,4124,4178,4278/binding site: carbohydrate (Asn) (covalent)
F:168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 76.5%; Score 39; DB 1; Length 4543;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOYGSSPCS 9
Db 1839 QOAGSNPCS 1847

RESULT 8
A25521
Ig kappa chain V region (321) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997
C:Accession: A25521
R:Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, B.Y.; Schrantz, R.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986
A:Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IgM
A:Reference number: A94135; MUID:87041448; PMID:3095834
A:Accession: A25521
A:Molecule type: DNA
A:Residues: 1-54 <CHE>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 48 QOYGSSP 54

RESULT 9
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37520
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <KLE>
A:Cross-references: EMBL:Z26612; NID:G405682; PIDN:CAA81365.1; PID:G405683
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 73 QOYGSSP 79

RESULT 10
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C:Accession: S67940
R:Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A:Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A:Reference number: S67940; MUID:92314301; PMID:1617110
A:Accession: S67940
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <HEX>
A:Cross-references: EMBL:X73852
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 74.5%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 71 QOYGSSP 77

RESULT 11
S37524
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37524
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37524
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26620; NID:G405690; PIDN:CAA81373.1; PID:G405691
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYGSSP 7
Db 73 QOYGSSP 79

RESULT 12
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37513
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37513
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26598; NID:G405688; PIDN:CAA81352.1; PID:G405669
C:Superfamily: immunoglobulin V region; immunoglobulin homology

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C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 73 QOYGSSP 79

RESULT 13

S37519
IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37519
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+)-IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 73 QOYGSSP 79

RESULT 14

S37517
IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+)-IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37517
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 73 QOYGSSP 79

RESULT 15

S37510
IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37510
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+)-IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37510
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26601; NID:g405662; PIDN:CAA81355.1; PID:g405663
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 74.5%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYGSSP 7
Db 73 QOYGSSP 79

Search completed: April 21, 2004, 17:38:30
Job time : 8.21739 secs